

**Amendments to the Drawings:**

The attached sheet of drawings includes changes to Figs. 1, 3, and 4. This sheet, which includes Figs. 1-16, replaces the original sheet including Figs. 1-16. In Figs. 1, 3, and 4, previously omitted SEQ ID NO:s have been added.

Attachment: Replacement Sheet

Annotated Sheet Showing Changes

**REMARKS/ARGUMENTS**


In the specification, the paragraph on page 27, beginning with line 20, has been amended to add the previously omitted SEQ ID NOs to each nucleotide sequence that is more than ten nucleotides in length. Appendices I and II have been replaced with new Appendices I and II, which merely add the previously omitted SEQ ID NOs to each nucleotide sequence that is more than ten nucleotides in length.

In amended Figure 1, the previously omitted SEQ ID NOs have been added to each nucleotide sequence more than ten nucleotides in length and to each amino acid sequences more than four amino acids in length. Similarly, in amended Figures 3 and 4, the previously omitted SEQ ID NOs have been added to each nucleotide sequence more than ten nucleotides in length.

Applicants respectfully request entrance of the above amendments. In view of the above remarks, early notification of a favorable consideration and allowance of all claims is respectfully requested.

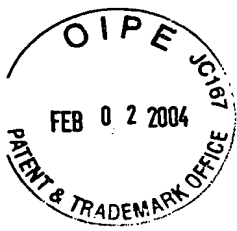
If after this amendment there are issues remaining which discussion could advance prosecution, Applicants respectfully request that the examiner call the undersigned attorney at the phone number listed.

Dated: February 2, 2004

Respectfully submitted,  
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Attachments



## Annotated Sheet Showing Changes

Figure 1  
~~FIGURE 1~~

ID-65

Clone 3-60

5 (SER ID No: 1)  
GTGTTTATGATGAAAAAAGGACAAGTAAATGATACTAAGCAA  
TCTTACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAA  
TTTTAGGGTCATTTCATAATGGTCACAAGTCCTGTTTTTGCGGA  
TCAAACACATCGGTTCAAGTTAATAATCAGACAGGCACTAG  
10 TGTGGATGCTAATAATTCTTCCAATGAGACAAGTGCGTCAAGT  
GTGATTACTTCCAATAATGATAGTGTTCAGCGTCTGATAAAG  
TTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTC  
CTTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTG  
AACAAGGGAATTATGTTTATAGCAAAGAAACCGAGGTGAAAA  
15 ATACACCTTCAAAATCAGCCCCAGTAGCTTTCTATGCAAAGA  
AAGGTGATAAAGTTTTCTATGACCAAGTATTTAATAAAGATA  
ATGTGAAATGGATTTTCATATAAGTCTTTTGGTGGCGTACGTCG  
ATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTTCA  
GACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAA  
20 TCAAGAGAAAATAGCAACGCAAGGAAATTATACATTTTCA  
TAAAGTAGAAGTAAAAAATGAAGCTAAGGTAGCGAGTCCAA  
CTCAATTTACATTGGACAAAGGAGACAGAATTTTTTACGACC  
AAATACTAACTATTGAAGGAAATCAGTGGTTATCTTATAAATC  
ATTCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAGCATCTT  
25 CAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAAC  
CACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAA  
CGAAACAACCTACAGGTTTTGATATTTTAATTACGAATATTAAA  
GATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTGGACTG  
AACAAGGAGGGCAAGATGATATTAAATGGTATACAGCTGTAA  
30 CTACTGGGGATGGCAACTACAAAGTAGCTGTATCATTGCTG  
ACCATAAGAATGAGAAGGGTCTTTATAATATTCATTTATACTA  
CCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACCTAA  
AGTGACAGTAGCTGGAACCTAATTCTTCTCAAGAACCTATTGA  
AAATGGTTTACCAAAGACTGGTGTTTATAATATTATCGGAAGT  
35 ACTGAAGTAAAAAATGAAGCTAAAATATCAAGTCAGACCCAA  
TTTACTTTAGAAAAAGGTGACAAAATAAATTATGATCAAGTA  
TTGACAGCAGATGGTTACCAGTGGATTTCTTACAAATCTTATA  
GTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAG  
TAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTA  
40 TCCCAACTTACCTAAAACAGGTACCTATACATTTACTAAAAC  
GTAGATGTGAAAAGTCAACCTAAAGTATCAAGTCCAGTGGAA  
TTTAATTTTCAAAAGGGTGAAAAAATACATTATGATCAAGTGT  
TAGTAGTAGATGGTCATCAGTGGATTTCATACAAGAGTTATTC  
CGGTATTCGTCGCTATATTGAAATTTAA

(SEQ ID NO: 2)

MFMMKKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNN  
QTGTSVDANNSSNETSASSVITSNNDSSVQASDKVVNSQNTATKDITPLVETK  
5 PMVEKTLPEQGNVYVYSKETEVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDN  
VKWISYKSFGGVRRYAAIESLDPSGGSETKAPTPVTNSGSNNQEKIATQGNYT  
FSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIEGNQWLSYKSFNGVRRFV  
LLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFDILITNIKDDNGIA  
10 AVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFADHKNEKGLYNIHLY  
YQEASGTLVGVTGTVAGTNSSQEPIENGLPKTG VYNIIGSTEVKNEAKISS  
QTQFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDE  
ATKPTSYPNLPKTGTYTFTKTVDVKSQPKVSSPVEFNFQKGGEKIHVDQVLVVD  
GHQWISYKSYSGIRRYIEI\*

15

Sequence description

A) Length: 1642 bp - 547 aa (full length gene)

B) Sequence Characteristics:

Potential leader peptide sequence

20

Orf is preceded by a potential Shine-  
Dalgarno sequence.

ID-66

25

Clone 3-5

(SEQ ID NO: 3)

ATGATATTGAGACGTCGAACTATTGTTTTATGGCAACTGGGTATCGCCATT  
TCTCTCATTCTTAGTATTCTAGCCTTAAATCTTTATTTCCATAGTACTCCCTT  
30 GCAAACCAATGCAGCTTTACGGAACCTTGCTCCTTCATTAAACCATCTTTTT  
GGGACAGATGGTTTAGGTAGGGATATGTTTGTGAGAACGATTAAAGGACT  
TTATTTCTCTCTACAAGTCGGCTTATTAGGTGCCCTTATGGGGGTCATTCTG  
GCGACAGTTTTTGGAGTGCTTGCAGGTTTAGGAAATAGCATTATTGATAAA  
ATAATAGCATGGTTAGTTGATTTGTTTATTGGTATGCCTCATTGATTTTAA  
35 TGATTCTCATTCTTTTGTGTTGGGAAAGGTGCTCAAGGGGTCATCATTGC  
AACGGCTGTTACACATTGGCCTTCTTTAGCAAGGCTTATCCGCAATGAAGT  
CTATCATCTAAAGAATAAAGAATTTGTCCAACCTTTCTAAAAGTATGGGAAA  
AACGCCTTATTATATTGTGAGGCATCATATCCTGCCTTTGATTGCTTCTCAA  
ATTTTCATTGGTTTTATCCTCTTATTTCCACATGTCATCCTACATGAAGCAT  
40 CAATGACTTTCTTAGGATTTGGGCTCTCTGCCGAACAACCTTCGGTTGGTA  
TCATTCTGTCAGAGGCAGCTAAGCATATCTCTCTTGGAAATTGGTGGTTGG  
TTATCTTTCCAGGACTTTATCTTATTTTGGTTGTCAATGCATTTGATACTAT  
CGGAGAATCTTTAAAGAACTCTTTTACCCTCAAACCTGATCATTTTTAG

(Seq ID No: 4)

MILRRRTIVLWQLGIAISLILSILALNLYFHSTPLQTNAALRNLAAPSLNHLFGTD  
GLGRDMFVRTIKGLYFSLQVGLLGALMGVILATVFGVLAGLGNSIIDKIIAWL  
VDLFIGMPHLIFMILISFVVGKGAQGVIIATAVTHWPSLARLIRNEVYHLKNKE  
5 FVQLSKSMGKTPYYIVRHHILPLIASQIFIGFILLFPHVILHEASMTFLGFGLSAE  
QPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTIGESLKKLFYPQTDHF  
\*

10 Sequence description

A) Length: 822 bp - 274 aa (full length gene)

B) Sequence Characteristics:

Potential leader peptide sequence

15 Orf is preceded by a potential Shine-  
Dalgarno sequence.

ID-78

20

Clone 3-5b

(Seq ID No: 5)

ATGACAGAAACATTATTAAGCATTAAAGACCTCTCCATCACCTTCACTCAA  
TACGGAAGATTTTAAAACCATTTCAATCAACACCGATACAAGCGCTGA  
25 ATTTAGAAATTAAAAAAGGTGAGTTATTAGCTATTATAGGTGCTAGTGGTT  
CGGGGAAGAGTTTATTAGCACATGCTATTATGGATATTCTTCCTAAAAATG  
CATCTGTAACAGGAGATATGATTTATCGTGGTCAATCACTAAATTCTAAAC  
GCATTAAACAGTTGCGAGGAAAAGATATTACGTTGATTCCACAATCAGTTA  
ATTATTTAGATCCATCTATGAAAGTCAAACATCAGGTGCGCTTAGGTATCT  
30 CAGAAAATTCAAAGGCTACTCAAGAAGGATTGTTTCAACAGTTTGGTTTAA  
AAGAAAGTGATGGTGACTTGGATCCTTTCCAACCTTCTGGCGGAATGCTCC  
GACGTGTTTTGTTTACAACGTGTATTAGTGATAAGGTTTCTTTGATTATTGC  
GGATGAGCCCACCCCTGGATTACATCCAGATGCTCTGCAAATGGTTTTAGA  
CCAACACTACGCTCCTTTGCAGATAAAGGAATAAGCGTTATATTTATCACTCA  
35 TGATATTGTAGCAGCTAGTCAAATTGCTGATCGTATTACTATTTTTAAAGA  
GGGAAAAGCTATTGAAACAGCTCCAGCTAGTTTCTTTAGCGGAAATGGAG  
AGCAGTTACAAACAGAATTTGCTAGAAAGTTTATGGCGCTCTCTCCACAGC  
AAGAATTTTTGAAAGGAGTTACTCATGACCTTAGAGGCTAA

40

(Seq ID No: 6)

MTETLLSIKDLSTFTQYGRFLKPFQSTPIQALNLEIKKGELLAIGASGSGKSL  
AHAIMDILPKNASVTGDMIYRGQSLNSKRIKQLRGKDITLIPQSVNYLDPSMK  
VKHQVRLGISENSKATQEGLFQQFGLKESDGDLDPFQLSGGMLRRVLFTTCIS  
DKVSLIIADEPTPGLHPDALQMVLDQLRSFADKGISVIFITHDIVAASQIADRITI  
FKEGKAJETAPASFFSGNGEQLQTEFARSLWRSLPQQEFLKGVTHDLRG\*

Sequence description

5

A) Length: 804 bp - 268 aa (full length gene)

B) Sequence Characteristics:

No obvious leader peptide sequence

10

Orf is preceded by a potential Shine-Dalgarno sequence.

This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified downstream and fully sequenced.

15

ID-79

Clone 3-5c

20

(SEQ ID NO: 7)

GTCCATCTGGGGTGGTTCCCGATTGGTATTTCTTCTCCGATAGGTACTTTGA  
GTCAAGATATTACGTTAGCTGATCGTATTAAGCACCTTATTTTACCTGTTTT  
CACGGTAAGTATTCTAGGCATTGCCAATGTAACCTCTTCATACTAGAACTAA  
AATGATGTCGGTACTTTCTAGTGAATATGTCTTATTTGCCAGAGCGCGTGG  
25 GGAAACGGAATGGCAAATTTTTAAAAATCATTGTCTTAGAAATGCTATCGT  
ACCAGCTATTACACTGCATTTTTCCTATTTTGGAGAATTGTTTGGAGGATCC  
GTTCTTGCTGAGCAAGTTTTCTCATATCCAGGACTAGGGTCTACCCTAACT  
GAAGCAGGACTTAAAAGTGATACACCGCTACTTCTAGCTATTGTGATGATA  
GGGACATTATTTGTTTTTGCGGGCAATCTTATTGCGGATATTTTAAATAGC  
30 ATAATCAATCCACAGTTAAGGAGAAAAGTATGA

30

(SEQ ID NO: 8)

VHLGWFPIGISSPIGTLSDITLADRIKHLILPVFTVSILGIANVTLHTRTKMMSV  
LSSEYVLFARARGETEWQIFKNHCLRNAIVPAITLHFSYFGELFGGSVLAEQVF  
SYPGLGSTLTEAGLKSDTPLLLAIVMIGTLFVFAGNLIADILNSINPQLRRKV\*

35

Sequence description

A) Length: 495 bp - 165 aa (partial gene sequence)

B) Sequence Characteristics:

40

N-terminus has yet to be determined.

This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified upstream.

ID-80

5

Clone 2-17

(SEQ ID NO: 9)

TTGCGGACAATTACGTTCAAACACAATGAAACGCGATCGTCAAAAAGCGA  
AGGTAGGGCGGTAATGCTTAAAAGATTATTTACTGAAGATGGGGAATTGA  
10 CAAAGATTAGTCGTCGTTTCGTTTGGATGTTAGTGGTTATCTATTGTCTTAT  
TATTGTCAGGATGTGTTTTGGGCCTCAAATTATGATTGAGGGGGTATCAAC  
TCCGAATGTTTCAGCGCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTAA  
TTCTTTTCGTAGTTTAGATCAGCTAACTAGCTTTAAAGAGATTTTTTGGGTT  
ATTGGTCAAAATGTAGTGAATATTTACTGCTGTTTCCTCTCATTATAGGGT  
15 TACTATCCCTAAAGCCAAGTTTACGGAAATATAAAAGCGTTATATTACTTG  
CTTTCTTGATGTCTCTTTTCATAGAGTGTACTCAAGTTGTTTTAGATATTTT  
AATAGATGCTAATCGGGTTTTTGAATCGACGATCTATGGACAAATACCTT  
AGGCGGTCCTTTCGCCCTATGGAGTTATCGAAACATAAAAGGTTGGCTTCT  
AACTATTAGAAAATGA

20

(SEQ ID NO: 10)

MRTITFKHNETRSSKSEGRAVMLKRLFTEDGELTKISRRFVWMLVVIYCLIIVR  
MCFGPQIMIEGVSTPNVQRFGRIVALLVPFNSFRSLDQLTSFKEIFWVIGQNVV  
NILLFPLIIGLLSLKPSLRKYKSVILLAFLMSLFIECTQVVLDILIDANRVFEIDD  
LWTNTLGGPFALWSYRNIKWLLTIRK\*

25

Sequence description

- 30 A) Length: 579 bp - 193 aa (full length gene)  
B) Sequence Characteristics:  
Possesses a potential leader peptide sequence  
No obvious Shine-Dalgarno, but the 'TTG' codon  
may not be the actual translation start point.  
A methionine (ATG) that occurs ~22 codons  
35 downstream of the 'TTG' is preceded by a  
potential Shine-Dalgarno sequence and may  
represent the actual start codon.

ID 81

40

Clone 3-1

(SEQ ID NO: 11)  
 TTGAAAAATTTAAATCGTTATGTAGTTGCGGTTTCTGGAGTCGTTTTACATT  
 TAATGCTAGGATCAACTTATGCTTGGAGTGTGTTTCGTAACCCAATTATCT  
 CAGAGACTGGTTGGGATATTTTCATCAGTTTCATTCGCTTTTAGTTTGGCTAT  
 TTTTGTCTAGGAATGTCTGCAGCTTTTATGGGACACTTAGTAGAGCGTTTT  
 5 GGTCCTAGGATAATGGGAATGATTTCTGCTATTTTATATGGAGCAGGGAAT  
 GTGTTAACAGGCTTAGCCATTGAAACTCAGCAGTTATGGTTACTGTATGTT  
 GCATACGGTATTTTAGGAGGAATCGGACTTGGTTCAGGTTATATTACTCCA  
 GTATCGACTATTATTAAATGGTTTCCTGATAGGAGGGGACTAGCAACAGG  
 ATTCGCTATTATGGGATTTGGCTTTGCTTCTTTAGTAACAAGTCCGCTTGCA  
 10 CAATCCTTACTGATTAGGATTGGTGTGGGTAAAACGTTTTATATTTTGGGA  
 TTAGTATATTTTTTTGTCATGATGATTGCCTCACAATTTATTAAACAACCAC  
 CTCAGGAAAAAATAACTATTTTGACTCACGATGGTAAAAAGAATGCTATG  
 AATTCACAAATTATCACTGGATTAAGCAACGTCGCTATAAAATCAAA  
 AACCTTTTACATCATTGGTTGACCTTGTTTATTAATATTTTCGTGTGGCTTA  
 15 GGTTTAATATCAGCAGCTTCACCAATGGCACAAGATTTAGCAGGCTATTCC  
 GCAGAATCTGCAGCCTTATTAGTAGGGGTACTAGGGGATTTAACGGTTTT  
 GGACGTCTGTTATGGGCAAGTCTCTCTGACTACATTGGACGCCCGTTGACC  
 TTTATAATATTATTTATTGTGAACCTTTATTATGACTTCTAGTTTATTTTTGTC  
 ATTCAATGCTATTGTATTTGCAATAGCGATGTCTATTTTAATGACTTGTTAT  
 20 GGTGCAGGTTTTTCCTTATTACCTGCTTATCTAAGTGATATTTTTGGAACAA  
 AGGAATTAGCTACTTTACATGGTTATAGTTTAACAGCATGGGCAATAGCAG  
 GTCTGTTTGGGCCCCCTATTGTTATCAAAGACATATTCATGGGGAAATTCCT  
 ATCAATTGACATTAATGGTTTTTTGGTTTTTTATTCTTATTCGGATTATTGTTA  
 TCTCTATATTTAAGAAAATTAACAACATAAGTTGTGTAG  
 25 (SEQ ID NO: 12)  
 LKNLNRYVAVSGVVLHMLGSTYAWSVFRNPIISETGWDISSVSFAFSLAIFC  
 LGMSAAFMGHLVERFGPRIMGMSAILYGAGNVLTGLAIETQQLWLLYVAYG  
 ILGGIGLGSYITPVSTIIKWFPDRRLATGFAIMGFGFASLVTSPLAQSLIRIG  
 VGKTFYILGLVYFFVMMIASQFIKQPPQEKITILTHDGKKNAMNSQIITGLKAN  
 30 VAIKSKTFYIIWLTFLFINISGLGLISAASPMQDLAGYSAESAALLVGVLGIFN  
 GFGRLLWASLSDYIGRPLTFIILFIVNFIMTSSLFLSFNAIVFAIAMSILMTCYGA  
 GFSLLPAYLSDIFGTELATLHGYSLTAWAIAGLFGPLLLSKTYSWGNSYQLTL  
 MVFGFLFLFGLLLSLYLRKLTTKV\*

35

Sequence description:

- 40 A] Length 1221 bp - 407 a.a (full length gene).  
 B] TTG start codon with Shine-Dalgarno sequence upstream. Obvious signal peptide, with hydropathy plot exhibiting many possible membrane spanning regions, indicating protein to be transmembrane.



5 ID-82

Clone 48

(SEQ ID NO: 13)  
10 ATGGCAGATAAAAAACAGAACATTTAAACTTGTAGGTGCAGGATCTTCTAG  
CACACAAGAAAAAATTGAAAAGCCTGCTCTTTCGTTTATGCAAGATGCGTG  
GCGTCGCTTGAAAAAAAACAAATTAGCAGTAGTTTCACTCTATTTATTAGC  
TCTTTTACTTACTTTTTCGTTAGCCTCAAATTTATTTGTAATCAGAAGGAT  
15 GCTAATGGGTTTGATTGCGAAAAAAGTAACGACATATCGCAACTTACCACCT  
AAATTGAGTTCAAACCTTCCTTTTGGGAATGGTAGCATTAAATCCATCA  
(SEQ ID NO: 14)  
MADKNRTFKLVGAGSSSTQEKIEKPALSFMQDAWRRLKKNKLAVVSLYLLA  
LLLTFSLASNLFVTQKDANGFDSKKVTTYRNLPPKLSSNLPFWNGSINPS

20

Sequence description:

A] Current length is 303 bp - 101 aa  
B] No obvious signal peptide but Shine  
25 Dalgarno sequence upstream of the ATG start  
codon. Not identified directly using the LEEP system but was found  
directly downstream of ID-34 described in WO 00/06736.

—————→

30 ID-83

Clone 98

(SEQ ID NO: 15)  
35 ATGAAAATAGTAGTACCAGTAATGCCTCGCAGTCTTGAAGAGGCTCAAGA  
AATAGATTTATCAAAATTTGATAGTGTTGATATTATTGAATGGCGAGCTGA  
TGCCTTACCAAAGGATGACATTATTAATGTAGCTCCAGCTATTTTTGAGAA  
ATTCGCAGGTCATGAAATTATTTTACTTTTCGTACAACGCGTGAAGGTGG  
40 TAATATTGTCTTATCTGATGCTGAGTATGTTGAGTTAATCCAGAAAATTAA  
TTCTATCTACAATCCAGATTATATTGATTTTGAGTATTTTTCACATAAAGAA  
GTTTTTCAAGAAATGCTAGAAATTTCCAAATTTAGTCCTGTCTTATCACAATT  
TTCAAGAGACACCGGAGAATATTATGGAGATATTTTCAGAATTAACAGCC  
CTAGCACCACGAGTTGTGAAAATCGCAGTAATGCCAAAGAATGAACAAGA

5 TGTCTTAGACGTTATGAATTACACTCGCGGTTTCAAGACTATTAATCCTGA  
TCAAGTTTATGCGACGGTATCTATGAGTAAAATTGGACGTATTTCTCGTTTT  
GCTGGTGATGTAACCTGGATCTAGTTGGACATTTGCATATTTAGATTTCATCT  
ATCGCACCCGGACAAATTACTATTTTCAGAGATGAAGCGTGTCAAAGCATT  
GCTTGACGCTGACTGA

(SEQ ID NO: 16)  
10 MKIVVPVMPRSLEEAEIDLSKFDSVDIIEWRADALPKDDIINVAPAIFEFKAG  
HEIIFTFRTTREGGNIVLSDAEYVELIQKINSIYNPDYIDFEYFSHKEVFQEMLEF  
PNLVLSYHNFQETPENIMEIFSELTALAPRVVKIAVMPKNEQDVLDVMNYTRG  
FKTINPDQVYATVSMKIGRISRFAGDVTGSSWTFAYLDSSIAPGQITISEMKRV  
KALLDAD\*

15 Sequence description:

A] Length 678 bp, 225 aa (full length gene)  
B] No obvious signal peptide, but there is a  
Shine Dalgarno immediately upstream of ORF.

20 ID-84

25 Clone RS-52

(SEQ ID NO: 17)  
ATGAAAGACTTATTTGCAACAACAGAAGCATCATCAAGGAAACAGGAACA  
AGATAGAATTGTCAATTACATAAAACAACATGTTGAGTTAACAAATGGTA  
ATCAAATAAAAAAATTGAGTTTATCGACTTTCAAAAAAATGAGATGACA  
30 GGTACATGGGGAATTTCTACTAAAATTAATGAACAATTTTCGATTAGTTTT  
TCTGAAGATAGAATTGGTGGTAAACTTAGAGCATTAGGATATCAACCGAA  
TGAAATAGGTTTTTCAAAGGACATCAATAGTAATAATCAAATGTTAATGA  
TATTGAAGTGATTTATATGAAGAAAGAATAG

(SEQ ID NO: 18)  
35 MKDLFATTEASSRKQEQRIVNYIKQHVELTNGNQIKKIEFIDFQKNEMTGTW  
GISTKINEQFSISFSEDRIGGKLRLALGYQPNEIGFSKDINSNNQNVNDIEVIYMK  
KE\*

40 Sequence description:

A] length: 333 bp - 111 aa (partial sequence)  
B] No obvious Shine Dalgarno sequence upstream  
of the ATG start codon, and no obvious signal  
peptide within the protein.

ID-85

5

Clone RS-53

(SEQ ID NO: 19)  
10 ATGAAAAAACGTATATGGTATTTGATAATAATAATCACAGTAATTTTAGGA  
GGACTAGCCATGAAAAACTTATTTGCAACAACAGAAGCATCATCAAGGAA  
ACAGGAACAAGATAGAATTGTCAATTACATAAAACAACATGTTGAGTTAA  
CAAATGGTAATCAAATAAAAAAAATTGAGTTTATCGACTTTCAAAAAAAT  
GAGATGACAGGTACATGGGGAATTTCTACTAAAATTAATGAACAATTTTCG  
15 ATTAGTTTTTCTGAAGATAGAATTGGTGGTAAACTTAGAGCATTAGGATAT  
CAACCGAATGAAATAGGTTTTTCAAAGGACATCAATAGTAATAATCA  
(SEQ ID NO: 20)  
MKKRIWYLIHITVILGGLAMKNLFATTEASSRKQEQDRIVNYIKQHVELTNGN  
QIKKIEFIDFQKNEMTGTWGIS TKINEQFSISFSEDRIGGKLRLALGYQPNEIGFSK  
20 DINSNNQ

Sequence description:

25 A] Length: 351 bp - 117 aa (Partial sequence)  
B] Obvious signal peptide and Shine Dalgarno  
sequence upstream of the ATG start codon.

30

ID-86

Clone ID-74

(SEQ ID NO: 21)  
35 ATGTCAAATCAATATGATTATATCGTTATTGGTGGAGGTAGT  
GCAGGCAGTGGTACCGCTAATAGGGCAGCCATGTATGGAGC  
AAAAGTCCTGTTAATTGAAGGTGGACAAGTAGGTGGAACCTG  
TGTTAACTTAGGTTGTGTACCTAAGAAAATCATGTGGTATGG  
TGCACAAGTTTCTGAGACACTCCATAAGTATAGFTCAGGTTA  
40 TGGTTTTGAAGCCAATAATCTTAGTTTTGATTTTACTACTCTA  
AAAGCTAATCGCGATGCTTACGTGCAGCGGTCTAGACAGTCG  
TATGCCGCTAATTTTGAGCGTAATGGGGTCGAAAAGATTGAT  
GGATTTGCTCGTTTTATTGATAACCATACTATTGAAGTGAATG  
GTCAGCAATATAAAGCTCCTCACATTACTATTGCAACAGGTG

GACACCCTCTTTACCCTGATATTATTGGAAGTGAACCTTGGTG  
 AGACTTCTGATGATTTTTTTGGATGGGAGACCTTACCAAATTC  
 TATATTGATTGTTGGGGCGGGCTATATCGCGGCAGAACTTGC  
 TGGAGTGGTTAATGAATTAGGCGTTGAAACCCATCTTGCATT  
 5 TAGAAAAGACCATATTCTACGCGGATTTGATGACATGGTAAC  
 AAGTGAGGTTATGGCTGAAATGGAGAAATCAGGTATCTCTTT  
 ACATGCTAACCATGTACCTAAATCTCTTAAACGCGATGAAGG  
 TGGCAAGTTGATTTTTGAAGCTGAAAATGGGAAAACGCTTGT  
 CGTTGATCGTGTAATATGGGCTATCGGCCGTGGACCAAATGT  
 10 AGACATGGGACTTGAAAATACCGATATTGTTTTAAATGATAA  
 AGATTATATCAAAACAGATGAATTTGAGAATACTTCTGTAGA  
 TGGCGTGTATGCTATTGGAGATGTTAATGGGAAAATTGCCTT  
 GACACCGGTAGCAATTGCAGCAGGTCGTCGCTTATCAGAAAG  
 ACTTTTAAATCATAAAGATAACGAAAAATTAGATTACCATAA  
 15 TGTACCTTCAGTTATTTTTACTCACCTGTAATTGGGACGGTA  
 GGACTTTCAGAAGCAGCAGCTATCGAGCAATTTGGAAAAGAT  
 AATATCAAAGTCTATACATCAACTTTTACCTCTATGTATACGG  
 CTGTTACCAGTAATCGCCAAGCAGTTAAGATGAAGCTCATAA  
 CCCTAGGAAAAGAGGAAAAAGTTATTGGGCTTCATGGTGTTG  
 20 GTTATGGTATTGATGAAATGATTCAAGGTTTTTCAGTTGCTAT  
 CAAAATGGGGGCTACTAAAGCAGACTTTGATGATACTGTTGC  
 TATTCACCCAACCTGGATCTGAGGAATTTGTTACAATGCGCTA  
 A  
 (SEQ ID NO: 22)  
 25 MSNQYDYIVIGGGSAGSGTANRAAMYGAKVLLIEGGQVGGTC  
 VNLGCVPKIMWYGAQVSETLHKYSSGYGFEANNLSFDFTTLK  
 ANRDAYVQSRQSYAANFERNGVEKIDGFARFIDNHTIEVNGQ  
 QYKAPHITATGGHPLYPDIIGSELGETSDDFFGWETLPNSILIVG  
 AGYIAAELAGVVNELGVETHLAFRKDHILRGFDDMTSEVMAE  
 30 MEKSGISLHANHVPKSLKRDEGGKLIFEAENGKTLVVDRVIWAI  
 GRGPNVDMGLENTDIVLNDKDYIKTDEFENTSVDGVYAIGDVN  
 GKIALTPVAIAAGRRLSERLFNHKDNEKLDYHNVPSVIFTHPVIG  
 TVGLSEAAAIEQFGKDNKVYTSTFTSMYTAVTSNRQAVKMKLI  
 TLGKEEKVIGLHGVGYGIDEMIQGFSAIKMGATKADFDDTVAI  
 35 HPTGSEEFVTMR\*

40

ID-87

Clone RS-55

(SEQ ID NO: 23)

5 ATGACAAAAAACATCTTAAAAACGCTTGCCTTGGCACTTACTACAGTATCA  
GTAGTGACATACAGCCAGGAGGTATATGGATTAGAAAGAGAGGAATCGGT  
CAAACAAGAACAAACCCAGTCAGCTTCAGAAGATGATTGGTTCTGAAGAAG  
ATAATGAGAGGAAAACAAATGTTTCTAAAGAGAATTCTACTGTTGATGAA  
ACAGTTAGTGATTTATTTTCTGATGGAAATAGTAATAACTCTAGTTCTAAA  
ACCGAGTCAGTGGTAAGTGACCCTAAACAAGTCCCCAAAGCAAAACCAGA  
10 GGTTACACAAGAAGCAAGCAATTCTAGTAATGATGCTAGCAAAGTAGAAG  
TACCAAAACAGGATACAGCTTCAAAAAAGGAACTCTAGAAACATCAACT  
TGGGAGGCAAAAGATTTTCGTAAGTCTAGAGGGGATACTTTAGTAGGTTTTTCA  
AAATCTGGAATTAATAAGTTATCTCAAACATCACACTTGGTTTTACCAAGT  
CATGCAGCAGATGGAAGTCAATTGACACAAGTAGCTAGCTTTGCTTTTACT  
15 CCAGATAAAAAGACGGCCATTGCAGAATATACAAGTAGGCTAGGAGAAA  
ATGGGAAACCGAGTCGTTTAGATATTGATCAGAAGGAAATTATTGATGAG  
GGAGAAATATTTAATGCTTACCAGTTGACTAAGCTTACTATTCCAAATGGT  
TATAAGTCTATTGGTCAAGATGCTTTTGTGGACAATAAGAATATTGCTGAG  
GTTAACCTTCCTGAGAGTCTCGAGACTATTTTCAGACTATGCTTTTGTCTACA  
20 TGTCTTTAAACAAGTAAAGTTACCAGATAACCTAAAGGTCATTGGAGAA  
TTAGCTTTTTTTTGATAATCAGATTGGTGGTAAGCTTTACTTGCCACGTCCT  
TGATAAAATTAGCAGAACGCGCTTTCAAATCTAATCGTATTCAAACAGTTG  
AATTTTTGGGAAGTAAGCTTAAGGTTATAGGAGAAGCAAGTTTTCAAGAT  
AATAATCTGAGGAATGTTATGCTTCCGGATGGACTTGAAAAAATAGAATC  
25 AGAAGCTTTTACAGGAAATCCAGGAGATGAACATTACAACAATCAGGTTG  
TATTGCGCACAAGGACAGGCCAAAATCCACATCAACTTGCGACTGAGAAT  
ACTTACGTCAATCCGGACAAATCATTGTGGCGTGCAACACCTGATATGGAT  
TATACCAAATGGTTAGAGGAAGATTTTACCTATCAAAAAAATAGTGTTACA  
GGTTTTTCAAATAAAGGCTTACAAAAGGTAAGACGTAATAAAAACTTAGA  
30 AATTCCAAAACAACACAATGGTATTACTATTACTGAAATTGGTGATAACGC  
TTTTCGCAATGTTGATTTTCAAAGTAAAACCTTTACGTAAATATGATTTGGA  
AGAAATAAAGCTCCCCTCAACTATTCGGAAAATAGGTGCTTTTGCTTTTCA  
ATCTAATAACTTGAAATCCTTTGAAGCAAGTGAAGATTTAGAAGAGATTA  
AAGAGGGAGCCTTTATGAATAATCGTATTGGAAGTCTAGACTTGAAAGAC  
35 AAAGTTATCAAAATAGGTGATGCTGCTTTCCATATTAATCATATTTATGCC  
ATTGTTCTTCCAGAATCTGTACAAGAAATAGGACGTTTCAGCTTTTCGACAA  
AATGGTGCGCTTCACCTTATGTTTATCGGAAATAAGGTTAAACAATTGGT  
GAAATGGCTTTTTTATCCAATAAACTGGAAAGTGTAATCTCTCTGAGCAA  
AAACAATTAAAGACAATTGAGGTCCAAGCTTTTTCGGATAATGCCCTTAGT  
40 GAAGTAGTCTTACCGCCAAATTTACAGACTATTCGTGAAGAGGCTTTCAA  
AGGAATCATTTGAAAGAAGTGAAGGGTTCATCTACATTATCTCAGATTACT  
TTTAATGCTTTTGATCAAAATGATGGGGACAAACGCTTTGGTAAGAAAGTG  
GTTGTTAGGACACATAATAATTCTCATATGTTAGCAGATGGTGAGCGTTTT  
ATCATTGATCCAGATAAGCTATCTTCTACAATGGTAGACCTTGAAAAGGTT

TTAAAAATAATCGAAGGTTTAGATTACTCTACATTACGTCAGACTACTCAA  
 ACTCAGTTTAGAGAAATGACTACTGCAGGTAAAGCGTTGTTATCAAAATCT  
 AACCTCCGACAAGGAGAAAAACAAAAATTCCTTCAAGAAGCACAAATTTT  
 CCTTGGTCGCGTTGATTTGGATAAAGCCATAGCTAAAGCTGAGAAGGCTTT  
 5 AGTGACCAAGAAGGCAACAAAGAATGGTCATTTGCTTGAGAGGAGTATTA  
 ACAAAGCGGTATTAGCTTATAATAATAGTGCTATTAAAAAAGCTAATGTTA  
 AGCGCTTGGAAAAAGAGTTAGACTTGCTGACAGATTTAGTCGAGGGAAAA  
 GGACCATTAGCGCAAGCTACAATGGTACAAGGAGTTTATTTATTAAAGAC  
 GCCTTTACCATTGCCAGAATATTATATCGGATTGAACGTTTATTTTGACAA  
 10 GTCTGGAAAATTGATTTATGCACTTGATATGAGTGATACTATTGGCGAGGG  
 AAAAAAGATGCATATGGTAATCCTATATTAAATGTTGACGAGGATAATG  
 AAGGTTATCATACCTTGGCAGTTGCCACTTTAGCTGATTATGAAGGTCTTT  
 ATATTAAAGATATTTTAAATAGTTCCCTTGATAAGATTAAAGCAATACGCC  
 AGATTCCTTTGGCAAAATATCATAGATTAGGAATTTTCCAAGCTATCCGAA  
 15 ATGCAGCGGCAGAAGCAGACCGATTGCTTCCTAAGACACCTAAGGGGTAC  
 CTAAATGAAGTCCCAAATTATCGTAAAAAACAAATGGAGAAAAATTTAAA  
 ACCAGTTGATTATAAAACGCCGATTTTTAATAAGGCTTTACCTAATGAAAA  
 GGTAGACGGTGATAGAGCGGCTAAAGGTCATAATATAAATGCGGAGACTA  
 ATAATTCTGTAGCTGTAACACCAATAAGGTCCGAGCAGCAATTACATAAGT  
 20 CACAGTCTGATGTAAATTTACCTCAAACAAGTTCTAAAAATAATTTTATAT  
 ACGAGATTCTAGGATACGTTAGTTTATGTTTGCTTTTCCTAGTAACTGCTGG  
 GAAAAAAGGAAAACGAGCAAGAAAATAA

(SEQ ID NO: 24)  
 MTKKHLKTLALALTTVSVVTYSQEVYGLEREESVKQEQTQSASEDDWFEEDN  
 25 ERKTNVSKENSTVDETVDLFSDGNSNNSSSKTESVVSDBPKQVPKAKPEVTQE  
 ASNSSNDASKVEVPKQDTASKKETLETSTWEAKDFVTRGDTLVGFSKSGINKL  
 SQTSHLVLP SHAADGTQLTQVASFAFTPDKKTAIAEYTSRLGENGKPSRLDIDQ  
 KEIIDEGEIFNAYQLTKLTIPNGYKSIGQDAFVDNKNIAEVNLPESLETISDYAF  
 AHMSLKQVKLPDNLKVIGELAFFDNQIGGKLYLPRHLIKLAERAFKSNRIQTV  
 30 EFLGSKLVIGEASFQDNNLRNVMLPDGLEKIESEAFNGPGEHYNNQVVL  
 TRTGQNPHQLATENTYVNPDKSLWRATPDMDYTKWLEEDFTYQKNSVTGFS  
 NKGLQKVRNRKNLEIPKQHNGITITEIGDNAFRNVDFQSKTLRKYDLEEIKLPS  
 TIRKIGAFQSNLKSFEASEDLEEIKEGAFMNNRIGTDLKDKLIKIGDAAFH  
 INHIYAIVLPESVQEIGRSAFRQNGALHLMFIGNKVKTIGEMAFLSNKLESVNL  
 35 SEQKQLKTIEVQAFSDNALSEVVLPNLQTIREEAFKRNLHLKEVKGSSTLSQITF  
 NAFDQNDGDKRFGKKVVVRTHNNSHMLADGERFIIDPKLSSTMVDLEKVL  
 KIIEGLDYSTLRQTTQTQFREMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGR  
 VDLDKAIKAEKALVTKKATKNHLLERSINKAVLAYNNSAIKKANVKRLEK  
 ELDLLTDLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA  
 40 LDMSDTIGEGQKDAYGNPILNVDEDNEGYHTLAVATLADYEGLYIKDILNSSL  
 DKIKAIRQIPLAKYHRLGIFQAIRNAAAEADRLPKTPKGYLNEVPNYRKKQM  
 EKNLKPVDYKTPIFNKALPNEKVDGDRAAKGHNINAETNNSVAVTPIRSEQQL  
 HKSQSDVNLPQTSSKNNFIYEILGYVSLCLLFLVTAGKKGKRARK\*

Sequence description:

- 5                   A] Length 3168 bp - 1056 aa (Partial sequence)  
                  B] Obvious signal peptide with Shine Dalgarno  
                  sequence upstream of the ATG start codon.

10               ID-88

Clone RS-56

15

(SEQ ID NO: 25)

GCAGGATACATCATGCACAAGCACGAGGCTATCGTGTCATGCTGGGGTCA  
ACCCAGGAAGACATGTCGGCACAAGCTGAAGATTTCTTTACAGTCTGTACA  
CAATAAAGAGACGGGTAAGAGCGCTTTTAATGACAAAGAACGACTAGCAA  
20 TT

(SEQ ID NO: 26)

AGYIMHKHEAIVSCWGQPRKTCRHKLKISLQSVHNKETGKSAFNDKERLAI

25               Sequence description:

- A] Length:153 bp - 51 aa (partial sequence)  
                  B] No signal peptide visible, insufficient  
                  sequence data to determine the presence of a  
30               Shine Dalgarno sequence.

35               ID-89

Clone RS-58

(SEQ ID NO: 27)

GTGTCATTTATGCAAAGAAAATCCTATTTAAAATCCATGAGTGTTCTTACT  
40 TTAACAGCTTGTCTTATATCAGGATATGTGGTTAAAGATATTGCTATGTTA  
CATGCAGTATCTGCCAGTGAGAAGAAAGCAAATAATGTCAGTCCGAGAGA  
AAATCTCTACAGGGCTGTCAATGATAATTGGCTAGCCAATACAAAACCTCA  
AACAAGGGCAGACTAGTGTTAATAGTTTTTCAGAAATTGAGGATAAATTA  
AAGCAACTGTTAGTGTCTGATATGGCTAAAATGGCCTCAGGAAAGATTGA

AACAAACCAATGATGAACAGAAAAAAATGGTTGCATACTATAAAACAAGGTA  
 TGGACTTTAAAACAAGAGATAAAAAATGGTCTCAAACCTCTAAAACCAGTT  
 TTACAAAAACTTGAAGCAGTCTCTTCAATGAAAGACTTTCAAAGTTTGGCC  
 5 CATGATTTTGTGATGAGTGGTTTTGTTTTACCATTTGGTTTGACTGTGGAAA  
 CCAATGCTCGAGATAATAGCCAAAAGCAATTGGTGCTTCGTCAAGCACCC  
 GCATTACTTGAATCACCTGACCAATATAAGAAGGGCAATAAAGAAGGTGA  
 GGCTAAATTATCAGCTTACCGTACTTCAGCAATGGCTTTGCTTAAACAAGC  
 TGGAAAAAGTAACATTGAAGATAGAAAACTAGTTAAACAAGCTATAGCAT  
 10 TTGATAGACTCTTATCAGAAAAAACGCAAGTTGATCAAAGTAAAATCACA  
 GCTGAAAGTGAGACAGCTGCGGGGCGATATAACCCTGAAAGTATGGAAAC  
 GGTTCAACAATTACGCCAAGGAATTTGACTTTAAAGAATTGATTGAAAAACT  
 AGTTGGGCCAACGAATAAGGCAGTCAATGTAGAAGATAAACTTATTTTA  
 AACAGGTTAATGATGTTATAAATAGTAAACAATTAGCCAATATGAAAGCA  
 TGGATGATGATTTCTATGCTAGTTGATCAATCAGATTTTCTAGGAGAACAA  
 15 AATCGTCAAGCAGCGAGTGCTTTTAAGAATGTTGCGTCTGGTTTGACTCAG  
 ATTGAATCGAAAGAAAAAATGCTTACACCCAATTAG

(Seq ID No. 28)  
 20 MSFMQRKSYLKSMVLTLTACLISGYVVKDIAMHLHAVSASEKKANNVSPREN  
 LYRAVNDNWLANTKLKQGQTSVNSFSEIEDKLKQLLVSDMAKMASGKIETTN  
 DEQKKMVAYYKQGMDFKTRDKNGLKPLKPVQLKLEAVSSMKDFQSLAHDF  
 VMSGFVLPFGLTVETNARDNSQKQLVLRQAPALLES PDQYKKGNGEKEAKLS  
 AYRTSAMALLKQAGKSNIEDRKLVKQAIAFDRLLEKTQVDQSKITAESETAA  
 25 GRYNPESMETVHNYAKEFDKELIEKLVGPTNKA VNVEDKTYFKQVNDVINS  
 KQLANMKAWMMISMLVDQSDFLGEQNRQAASAFKNVASGLTQIESKEKMLT  
 PN\*

30 Sequence description:

A) Length: 1095 bp - 365 aa (full length gene)  
 B) an GTG (possible ATG start codon located 7 bp  
 further downstream) start codon with an obvious  
 35 signal peptide. Shine Dalgarno sequence present  
 upstream of the ORF.

ID-90  
 40

Clone RS-59



(SEQ ID NO: 29)

ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTTAAATGAG  
TATTGATAAACTTAGATATAAAGAACCAGAGAGTGAACATGACAAGCGAC  
CTACTTTTTATTGTTAGTACTTATACTTGTTACTGTAGCAGTTATATTGTC  
GTTATTTAAATATTTTTTATAG

5

(SEQ ID NO: 30)

MEMPKRNELLNKEIKMSIDKLRYKEPESEHDKRPTFYLVVLILVTVAVILSLFK  
YFL\*

10 Sequence description:

A] Length: 174 bp - 58 aa(full length gene)

B] No obvious signal peptide, but Shine

Dalgarno sequence is present upstream of ATG  
start codon.

15

20 ID-91

Clone RS-62 (partial sequence)

25

(SEQ ID NO: 31)

ATGCAGGTATTTTAAATATTGTCAATAAATTCTTTGATCCAGTTATTCATA  
TGGGTTCTGGGAGTTGTGATGCTAATTGTCATGACAGGTTTAGCCATGATAT  
TTGGAGTGAAGTTTTCTAAAGCACTTGAAGGTGGTAT

30

(SEQ ID NO: 32)

MQVFLNIVNKFFDPVIHMGSGVVMLIVMTGLAMIFGVKFSKALEGG

Sequence description:

35

A] Length: 141 bp - 41 aa (partial sequence

B] Shine Dalgarno sequence present upstream of  
ATG start codon with a possible signal peptide  
present

40

ID-92

Clone RS-69 (partial sequence)

(SEQ ID NO: 33)

5 ATGAAAAAGAAAACATTCAGTGCTTATAACTTTTTAACGGCTCTTATCCTT  
TGTCTTTTGACAGTGCTTTTATCTTTCCATTTTATTGGATTATGACAGGAG  
CTTTTAA

(SEQ ID NO: 34)

MKKKTFSAYNFLTALILCLLTVLFIFPFYWIMTGAF

10

Sequence description:

A] Length: 110 bp -36 aa (Partial sequence)

15

B] Possible signal peptide with Shine Dalgarno  
sequence directly upstream of the ATG start  
codon.

20

ID-93

Clone RS-70

25

(SEQ ID NO: 35)

30 ATGACTGAGAACTGGTTACATACTAAAGATGGTTCAGATATTTATTATCGT  
GTCGTTGGTCAAGGTCAACCGATTGTTTTTTTACATGGCAATAGCTTAAGT  
AGTCGCTATTTTGATAAGCAAATAGCATATTTTCTAAGTATTACCAAGTT  
ATTGTTATGGATAGTAGAGGGCATGGCAAAAGTCATGCAAAGCTAAATAC  
CATTAGTTTCAGGCAAATAGCAGTTGACTTAAAGGATATCTTAGTTCATTT  
AGAGATTGATAAAGTTATATTGGTAGGCCATAGCGATGGTGCTAATTTAGC  
TTTAGTTTTTCAAACGATGTTTCCAGATATGGTTAGAGGGCTTTTGCTTAAT  
35 TCAGGGAACCTGACTATTCATGGTCAGCGATGGTGGGATATTCTTTTAGTA  
AGGATTGCCTATAAATTCCTTCACTATTTAGGGAAACTCTTCCGTATATG  
AGGCAAAAAGCTCAAGTTATTTTCGCTTATGTTGGAGGATTTGAAGATTAGT  
CCAGCTGATTTACAGCATGTGTCAACTCCTGTAATGGTTTTGGTTGGAAAT  
AAGGACATAATTAAGTTAAATCATTCTAAGAACTTGCTTCTTATTTTCCA  
AGGGGGGAGTTTTATTCTTTAGTTGGCTTTGGGCATCACATTATTAAGCAA  
40 GATTCCCATGTTTTTAATATTATTGCAAAAAGTTTATCAACGATACGTTG  
AAAGGAGAAATTGTTGAAAAAGCTAATTGA

(SEQ ID NO: 36)

MTENWLHTKDGSDIYYRVVGQGQPIVFLHGNSLSSRYFDKQIAYFSKYYQVIV  
MDSRGHGKSHAKLNTISFRQIAVDLKDILVHLEIDKVILVGHSDGANLALVFQ

TMFPDMVRGLLLNSGNLTIHGQRWWDILLVRIAYKFLHYLGKLFPMRQKA  
QVISLMLEDLKISPADLQHVSTPVMVLVGNKDIIKLNHKKLASYPFRGEFYSL  
VGFGHHIIKQDSHVFNIIAKKFINDTLKGEIVEKAN\*

5

Sequence description:

- 10                   A] Length: 744 bp - 248 aa (full length gene)  
                    B] No obvious signal peptide, but Shine  
                    Dalgarno sequence upstream of the ATG start  
                    codon.

15

ID-94

20                   Clone RS-71

25

*(SEQ ID NO: 37)*  
ATGGTAGCAAAAAGAGTTAGGTAAAAATAGCTTTACTATCCCAACTATTTGT  
TCTAATTGCTCCGCAGGTACTGCCATTGCAGTTGTATATAATGATGACCAT  
TCTTTCTTAAGATACGGCTATCCCGAGTCTCCACTTCATATTTTTATCAATA  
CACGGATCATTGCACAGGCACCAAGCAAATATTTTTGGGCTGGTATTGGGG  
ACGGTATTTCAAAAAGCCCCTGAAGTAGAACGTGCTACCTTAGAGGCTAAG  
ACCAATAAACTACCACATACTGCAGTGTTAGGACAAGCAGTCGCTCTGTCT  
TCAAAGGAAGCTTTTTATCAATTTGGTGAACAAGGTCTAAAAGACGTTGAA  
GCTAATTTAGCTTCGCGTGCAGTTGAAGAAATTGCGCTTGATATCTTA

30

*(SEQ ID NO: 38)*  
MVAKELGKNSFTIPTICSNCSAGTAIAVVYNDHHSFLRYGYPEsplHIFINTRIIA  
QAPSKYFWAGIGDGIKAPEVERATLEAKTNKLPHTAVLGQAVALSskeafY  
QFGEQGLKDVEANLASRAVEEIALDIL

35

Sequence description:

- 40                   A] Length: 405 bp - 135 aa (Partial sequence)  
                    B] No obvious Shine Dalgarno sequence upstream  
                    of the ATG start codon, probable signal  
                    peptide present at the N-terminus.

ID-95

Clone RS-73

5 (SEQ ID NO: 39)  
TTGAGGGAACTTACTGGAAAATTTCAAGCGATTGCGATAAAATAAATCTT  
GCAGAGTTTTCTAGAGAAAGGAGGTCAGATTTATTGGAGTGGCAAGATCT  
AGCGCAGTTACCTGTATCTATTTTTTAAAGACTATGTTACAGATGCTCAAGA  
CGCGGAAAAACCTTTTATATGGACAGAAGTATTTTAAAGGGAGATTAATCG  
CTCAAATCAAGAAATTATTTTGCATATTTGGCCGATGACTAAGACAGTCAT  
10 TCTGGGGATGTTAGATCGAGAATTACCACATTTAGAATTAGCTAAAAAAG  
AAATCATCAGTCGTGGTTATGAACCAGTTGTTCCGAATTTTGGAGGTCTCG  
CAGTTGTAGCTGATGAAGGAATTTTAAATTTTTCATTGGTTATTCCAGATGT  
TTTTGAGAGAAAATTGTCTATCTCAGATGGGTATCTTATAATGGTCGATTTT  
ATTAGAAGTATATTTTCGGATTTTATCAACCTATTGAGCACTTTGAAGTA  
15 GAGACCTCCTATTGTCCTGGTAAGTTTGATCTTAGTATAAATGGCAAAAAA  
TTTGCTGGCTTGGCTCAGCGCCGTATAAAGAATGGTATTGCGGTATCAATT  
TACCTTAGCGTTTGTGGCGATCAAAAAGGGCGGAGTCAAATGATTTTCAGAT  
TTTTATAAGATTGGTCTAGGTGATACGGGTAGTCCAATTGCTTATCCAAAT  
GTAGATCCTGAAATTATGGCTAATCTATCTGATCTATTAGATTGTCCTATG  
20 ACAGTAGAAGATGTTATTGATCGTATGTTGATTAGCCTTAAACAAGTAGGT  
TTTAATGATCGTTTACTGATGATTAGACCCGATTTAGTTGCAGAGTTTGAT  
AGATTTTCAGGCTAAGTCTATGGCTAATAAGGGGATGGTGAGCAGAGATGA  
ATAA  
  
25 (SEQ ID NO: 40)  
MRETYWKISSDCDKINLAEFRERRSDLLEWQDLAQLPVSIFKDYVTDAQDAE  
KPFITWTEVFLREINRSNQEIILHIWPMKTVILGMLDRELPHLELAKKEIISRGYE  
PVVRNFGGLAVVADEGILNFSLVIPDVFERKLSISDGYLIMVDFIRSIFSDFYQPI  
EHFEVETSYCPGKFDLSINGKKFAGLAQRRRIKNGIAVSIYLSVCGDQKGRSQMI  
30 SDFYKIGLGDTSPIAYPNVDPEIMANLSDLLDCPMTVEDVIDRMLISLKQVGF  
NDRLLMIRPDLVAEFDRFQAKSMANKGMVSRDE\*

Sequence description:

35 A) Length: 921 bp -307 aa (Full-length gene sequence)  
B) No obvious Shine Dalgarno sequence upstream  
of the TTG start codon or signal peptide  
visible. Actual start point may be a further  
40 85 bp downstream (TTG). This start point is  
preceded by a typical Shine-Dalgarno sequence.

ID-96

Clone RS-74

5

(SEQ ID NO: 41)

TTGGAAGGTTTACTTATTGCATTGATTCCCATGTTTGCCTGGGAAAGTATT  
GGATTTGTTAGTAATAAAAATTGGAGGGCGTCCAAATCAACAAACATTTGG  
AATGACTTTAGGAGCATTGCTATTTGCGATTATCGTATGGTTATTTAAACA  
10 GCCAGAGATGACTGCCTCATTGTGGATTTTGGTATCTTAGGTGGTATCCT  
ATGGTCAGTCGGCCAAAATGGTCAATTTCAAGCAATGAAATATATGGGAG  
TCTCTGTTGCTAATCCACTGTCAAGTGGTGCACAATTAGTAGGTGGAAGCC  
TAGTTGGTGCTTTAGTCTTTCATGAATGGACTAAGCCAATCCAATTTATTTT  
AGGATTGACAGCGTTGACATTATTAGTTATCGGCTTCTATTTCTCAAGTAA  
15 ACGTGATGTTTCAGAACAAGCTTTGGCAACACATCAAGAGTTTTCAAAAG  
GATTTGCTACAATTGCTTATTCAACTGTAGGTACATCTCGTACGCAGTTT  
ATTTAACAACATTATGAAGTTCGACGCTATGGCCGTCATTTTACCCATGGC  
TGTTGGAATGTGTCTAGGTGCAATTTGTTTCATGAAGTTTCGTGTAACTTT  
GAGGCTGTTGTTGTTAAAAATATGATTACAGGTCTCATGTGGGGCGTTGGT  
20 AATGTCTTCATGTTATTGGCAGCAGCTAAAGCAGGGCTAGCAATTGCTTTT  
AGTTTTTCTCAACTTGGAGTAATTATCTCTATTATTGGTGGTATTTTATTTT  
AGGTGAGACAAAAACGAAGAAAGAGCAGAAATGGGTGTCATGGGTATC  
CTTTGTTTTGTTATGGGTGCTATATTACTTGGTATTGTTAAATCTTATTAA

(SEQ ID NO: 42)

25 MEGLLIALIPMFAWESIGFVSNKIGGRPNQQTFGMTLGALLFAIIVWLFKQPEM  
TASLWIFGILGGILWSVGQNGQFQAMKYMGVSVANPLSSGAQLVGGSLVGAL  
VFHEWTKPIQFILGLTALTLLVIGFYFSSKRDVSEQALATHQEFSKGFATIAYST  
VGYISYAVLFNNIMKFDAMAVILPMAVGMCLGAICFMKFRVNFEAVVVKNMI  
TGLMWGVGNVFMLLAAAKAGLAIAFSFSQLGVIIIGGILFLGETKTKKEQK  
30 WVVMGILCFVMGAILLGIVKSY\*

Sequence description:

35

A] Length: 867 bp - 289 aa (full-length gene)  
B] Possible Shine Dalgarno sequence upstream of  
GTG start codon, no obvious signal peptide  
present.

40

ID-97

Clone RS-75

(SEQ ID NO: 43)  
5 ATGACAACTTACTACGAAGCTATAAACTGGAACGAAATTGAAGATGTTAT  
TGATAAATCAACTTGGGAAAACTAACCGAACAATTTTGGCTCGATACAC  
GTATCCCTTTATCAAATGACTTAGACGATTGGCGCAAACCTTCCGCTCAAG  
AAAAAGATCTTGTTGGCAAGGTTTTTGGAGGCTTAACCCTACTTGATACCA  
TGCAATCAGAACTGGTGTGAAGCTATTCGTGCCGATGTTTCGCACGCCTC  
10 ACGAAGAAGCTGTCTTAAACAATATTCAATTCATGGAATCTGTTACGCTA  
AATCTTATTCTTCAATTTTCTCAACTTTAAATACTAAATCAGAAATTGAAG  
AAATTTTCGAGTGGACTAATAATAATGAGTTCCTTCAAGAAAAAGCACGT  
ATTATCAATGACATTTATGCTAATGGAAATGCCCTTCAAAAAAGGTGGCT  
TCCACCTACCTCGAACTTTCCTTTTTTATTCTGGCTTTTTCACACCTCTTTA  
CTATTTGGGAAATAATAAGTTAGCAAATGTTGCTGAAATCATTAAATTAAT  
15 TATTCGTGATGAATCTGTACATGGTACTTATATCGGTTACAAATTCCAGCTT  
GGTTTTAACGAATTACCAGAAGATGAGCAAGAGAATTTTCGTGATTGGAT  
GTATGACCTCCTTTATCAGCTGTATGAAAACGAAGAAAAATACACCAAGA  
CACTTTATGATGGCGTAGGATGGACTGAAGAAGTTATGACCTTTTTACGCT  
ACAATGCTAATAAAGCTCTTATGAATTTAGGACAAGATCCTTTATTCCAG  
20 ATACAGCAAATGATGTCAACCCAATTGTTATGAATGGTATTTCAACAGGAA  
CATCAAACCATGACTTCTTCTCTCAAGTAGGTAATGGTTACCTACTTGGTA  
GCGTTGAAGCTATGCATGATGACTATAACTATGGATTATAA  
(SEQ ID NO: 44)  
25 MTTYEAINWNEIEDVIDKSTWEKLTEQFWLDTRIPLSNDLDDWRKLSAQEK  
DLVGKVFGGLTLLDTMQSETGVEAIRADVTPHEEAVLNNIQFMESVHAKSY  
SSIFSTLNTKSEIEEIFEWTNNNEFLQEKARIINDIYANGNALQKKVASTYLETF  
LFYSGFFTPLYYLGNKLANVAEIIKLIIRDES VHGTYIGYKFQLGFNELPEDEQ  
ENFRDWMYDLLYQLYENEEKYTKTLYDGVGWTEEVMTFLRYNANKALMNL  
30 GQDPLFPDTANDVNPIVMNGISTGTSNHDFFSQVGNGYLLGSVEAMHDDYN  
YGL\*

Sequence description:

35 A] Length: 960 bp - 320 aa (full length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, but no signal peptide  
present.

40

ID-98

Clone RS-77 (partial sequence)

(SEQ ID NO: 45)  
5 ATGAATTGGTCACGTATCTGGGAACTCGTAAAAATTAATATCCTTTATTCA  
AACCCTCAGACTCTATCGGCACTAAGAAAAAAGCAAGAAAAGCATCCTAA  
AAAAGAATTTTCAGCTTATAAATCCATGTTTAGAAATCAGTTATTTTCAGAT  
TTTGCTCTTTTCAATAATTTATGTATTTCTCTTTGTATCACTTGATTTTAAAG  
AATATCCGGGCTATTTACGTTCTACATTGGTATCTTTACACTAGTATCCAT  
10 TATCTACTCTTTTATTGCGATGTACAGTGTTTTCTATGAGAGTGACGATGTT  
AA

(SEQ ID NO: 46)  
MNWSRIWELVKINILYSNPQTLSALRKKQEKHPKKEFSAYKSMFRNQLFQILL  
FSIIVFLFVSLDFKEYPGYFTFYIGIFTLVSIYSFIAMYSVFYESDDV

15  
Sequence description:

20 A] Length: 311 bp - 103 aa (Partial sequence)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, no obvious signal peptide at  
N-terminus.

ID-99

25  
Clone RS-78 (partial sequence)

(SEQ ID NO: 47)  
30 TAATCTTTTAGTCAACGGAGCAACAGGAAAATTGCAGGCTATGCGACAGA  
TATCCACCACATAATTTAGCAGAAGTCATTGATGCTGTCGTGTACATGAT  
TGATCACCTAAAGCTAAATTAGATAAATTAATGGAATTTCTACCTGGTCC  
AGATTTTCCAACCTGGCGCTATCATTCAAGGAAAAGATGAAATTCGTAAGG  
CATATGAGACTGGTAAGGGGAGAGTAGCGGTTTCGCTCGCGAACTGCTATT  
GAAACCTTAAAAGGTGGTAAGAAACAAATTATTGTTACTGAAATTCCTTAT  
35 GAAGTTAAT

(SEQ ID NO: 48)  
SFSQRSNRKIAGYATDIPPHNLAEVIDAVVYMIDHPKAKLDKLMEFLPGPDFPT  
GAIQKGKDEIRKAYETGKGRVAVRSRTAIETLKGGKKQIIVTEIPYEVN

40  
Sequence description:

A] Length: 312 bp - 104 aa (Partial sequence)  
B] No obvious Shine Dalgarno sequence or a

signal peptide. Both N- and C- termini of ORF  
yet to be elucidated.

5 ID-100

Clone RS-79

10 (SEQ ID NO: 49)  
ATGGGACGTAAGTGGGCCAATATTGTTGCCAAAAAGACTGCTAAAGATGG  
TGCTAACTCAAAAGTATACGCTAAATTCGGTGTTGAAATATATGTTGCTGC  
AAAGCAAGGTGAACCAGACCCCGAGTCAAACCTCAGCTCTAAAATTCGTTT  
TGGACCGTGCTAAGCAAGCACAAAGTTCCAAAGCATGTTATTGATAAAGCG  
15 ATTGATAAAGCCAAAGGAAACACAGATGAAACTTTCGTAGAGGGGACGCTA  
TGAAGGTTTTGGTCCAAATGGTTCAATGATTATTGTGGATACTTTGACATC  
AAATGTTAACCCTACGGCAGCAAATGTACGTACTGCTTACGGTAAGAACG  
GTGGCAATATGGGAGCTTCAGGATCGGTATCCTACTTATTTGATAAAAAAG  
GTGTCATCGTTTTTGGTGGTGATGATGCTGACACTGTCTTCGAACAATTACT  
20 TGAAGCGGATGTAGACGTAGATGATGTTGAAGCAGAAGAGGGAACAATA  
ACAGTTTATACCGCCCCAACAGATCTTCATAAAGGTATCCAAGCACTTCGC  
GATAATGGTGTAGAAGAATTCCAAGTTACTGAACTTGAAATGATTCCTCAA  
TCAGAAGTAGTATTGGAAGGTGATGACCTTGAACTTTTGAAAAGCTT  
25 (SEQ ID NO: 50)  
MGRKWANIVAKKTAKDGANSKVYAKFGVEIYVAAKQGEPPESNSALKFVL  
DRAKQAQVPKHVIDKAIDKAKGNTDETFVEGRYEGFGPNGSMIIVDTLTSNV  
NRTAANVRTAYGKNNGNMGASGSVSYLFDKKGVIVFAGDDADTVFEQLLEA  
DVDVDDVEAEEGTITVYTAPDLHKG IQALRDNGVEEFQVTELEMIPQSEVVL  
EGDDLETFEKL

30

Sequence description:

35 A] Length: 654 bp - 218 aa (Partial sequence)  
B] Possible Shine Dalgarno sequence upstream  
of ATG start, no obvious signal peptide

40 ID-101

Clone RS-80



(SEQ ID NO: 51)

TTGGAGAAATATTTGAAGAACCCGATTACATGGATTGGATTAGTTCTTGTG  
GTTACGTGGTTTTTAACTAAAAGTAGTGAATTTTGGTGTGTGTG  
TCTTGTGTAGTATTTGCTAGTCAAAGTGAT

5

(SEQ ID NO: 52)

MEKYLKNPITWIGLVLVVTWFLTKSSEFLIFGVCVLLLVFASQSD

Sequence description:

10

A] Length: 135 bp - 45 aa (partial sequence)  
B] Shine Dalgarno sequence upstream of TTG  
start codon with possible signal peptide  
evident at N-terminus.

15

ID-102

20

Clone RS-81

(SEQ ID NO: 53)

ATGACACAATCAGATGCATATCTCTCGTTGAACGCGAAGACACGCTTTAGA  
GATCGCACAGGTAATTATCATTTTACTTCGGATAAAGAGGCTGTTGAACAA  
TATATGATAGAACATGTTGAACCTAATACGATGGTGTTCACATCACTAATT  
GAAAAGCTAGATTATTTGGTTTCTAATACTACTATGAATCGGACCTTCTA  
AAACAATATAACCTTGAGTTTATTTGCCAAATTTTGGAGCATGCATACGCT  
AAGAAATTTGCTTTTCTAAATTTTATGGGGGCTTTAAAATTTTATAATGCTT  
ATGCTCTTAAT

25

30

(SEQ ID NO: 54)

MTQSDAYLSLNAKTRFRDRTGNYHFTSDKEAVEQYMIEHVEPNTMVFTSLIE  
KLDYLVSNYYESDLLKQYNLEFICQIFEHAYAKKFAFLNFMGALKFYNAYA  
LN

35

Sequence description:

40

A] Length: 318 bp - 106 aa (Partial sequence)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, no obvious signal peptide

## Clone 2-11A

5

(SEQ ID NO: 55)

ATGGTATTTATGGCAAATAAGAAAAAACAAGGAAAGAAAAACCAGAA  
GACCTACTAAGGCAGAAATAGAGCGTCAAAGAGCTATTCAAAGGATGATT  
ACTGCTCTTGTTTTAACAATTATTCTCTTCTTTGGTATTATCAGATTAGGTA  
10 TTTTGGTATTACAGTCTATAACGTCATCCGTTTTATGGTAGGTAGCTTGGC  
TTACTTATTTATTGCGGCAACTTTAATCTACCTTTATTTCTTTAAATGGTTG  
CGAAAGAAAGATAGCTTAGTAGCAGGTTTTTTGATAGCTTCTTTAGGATTA  
TTGATTGAGTGGCATGCTTACCTTTTCTCAATGCCTATTTTGAAAGATAAA  
GAAATTTTTCGTTCAACTGCTCGATTAATTGTGTCTGATTTAATGCAATTTA  
15 AAATCACTGTTTTTGCCGGTGGAGGTATGTTGGGTGCTTTGATTTACAAGC  
CAATTGCTTTTCTCTTTTCTAATATTGGTGCCTATATGATTGGTGTCTCTTC  
ATCATTTTGGGTCTCTTTTAAATGAGTTCTCTGGAAGTTTATGACATCGTCG  
AATTTATTAGAGCTTTTAAAAATAAAGTGGCAGAGAAGCACGAGCAAAAT  
AAAAAGGAGCGTTTTGCTAAGCGAGAGATGAAAAAAGCAATCGCTGAACA  
20 AGAGCGCATAGAGCGTCAAAAAGCTGAAGAAGAAGCTTATTTAGCTTCGG  
TTAATGTAGACCCTGAAACGGGTGAGATTCTAGAGGATCAAGCTGAGGAC  
AATTTGGATGATGCGCTACCACCTGAGGTAAGTGAAACATCAACTCCGGT  
ATTTGAGCCAGAGATCCTTGCTTATGAGACATCGCCTCAAAATGATCCTTT  
ACCAGTAGAGCCGACAATTTATTTAGAAGACTATGATTGCGCGATTCCCTAA  
25 TATGAGAGAAAATGATGAGGAAATGGTTTATGATTTAGATGATGATGTAG  
ATGATAGTGATATAGAAAATGTCGACTTTACACCTAAAACGACACTGGTTT  
ATAAATTACCAACGATAGATTTATTTGCACCAGATAAGCCTAAAAATCAAT  
CCAAAGAAAAGGATTTAGTCCGAAAGAATATCAGAGTTTTAGAAAGAAACA  
TTTAGAAGTTTTGGTATCGATGTAAAAGTAGAACGTGCTGAAATTGGACCA  
30 TCAGTTACTAAATATGAAATTAACCAGCAGTTGGAGTTCGTGTGAATCGT  
ATTTCAAATCTATCTGACGACCTAGCTCTTGCTCTTGCAGCAAAAGATGTG  
CGTATAGAAGCACCAATTCCTGGAAAATCATTAAATAGGTATTGAAGTTCCT  
AACTCAGAAATTGCAACGGTTTTCTTTCCGCGAACTTTGGGAACAATCTGAT  
GCCAATCCTGAAAACCTTTTAGAAGTACCACTAGGAAAAGCTGTTAACGG  
35 CAATGCTCGCAGTTTTAACTTAGCTAGAATGCCGCATCTTTTGGTAGCTGG  
TTCAACTGGTTCAGGTAAATCTGTGGCAGTTAATGGAATTATTTCAAGTAT  
TTTGATGAAGGCACGTCCAGATCAAGTTAAGTTTATGATGATTGATCCCAA  
AATGGTTGAATTATCTGTTTATAATGATATTCCACATTTATTAATCCCTGTT  
GTAACCAATCCGCGTAAAGCAAGTAAGGCACTCCAAAAAGTTGTTGATGA  
40 AATGGAAAATCGATACGAGTTATTTAGCAAAATTGGTGTGCGTAATATAG  
CAGGTTATAATACAAAGGTTGAAGAGTTTAATGCTTCCTCTGAGCAAAAAC  
AAATGCCTTTGCCTTTAATCGTTGTCATTGTAGATGAATTGGCTGACTTGAT  
GATGGTTGCTAGTAAAGAAGTTGAAGATGCTATTATTCGTTTGGGGCAAAA  
AGCACGTGCTGCAGGTATCCATATGATTCTTGCAACTCAACGTCCATCCGT

AGATGTTATTTCTGGTTTGATTAAAGCAAATGTTCCGTCGCGTATTGCATTT  
GCTGTTTCAAGTGGTACTGATAGCCGTACGATCCTTGATGAAAATGGTGCT  
GAAAAGCTCTTGGGACGGGGTGACATGCTCTTTAAGCCTATTGATGAGAAT  
CATCCAGTACGACTACAAGGTTCTTTATTTTCAGATGATGATGTTGAAAGG  
5 ATCGTTGGTTTTATCAAAGACCAAGCCGAGGCTGACTATGATGATGCCTTT  
GATCCTGGAGAAGTATCTGAAACAGATAACGGCTCTGGTGGTGGCGGCGG  
AGTACCTGAAAGTGATCCTCTTTTTGAAGAAGCCAAGGGACTCGTTTTAGA  
GACGCAAAAAGCAAGTGCCTCAATGATTCAACGCCGATTGTCTGTTGGTTT  
CAATAGAGCAACAAGACTAATGGAAGAATTAGAAGCAGCGGGGGTTATTG  
10 GTCCAGCAGAAGGAACCAAGCCACGAAAAGTTTAAATGACTCCAACCTCCG  
AGTGAATAA

(SEQ ID NO: 56)  
MVFMANKKKTKGKKTRRPTKAEIERQRAIQRMITALVLTIILFFGIIRLGIFGIT  
VYNVIRFMVGSLAYLFIAATLIYLYFFKWLRKKDSL VAGFLIASLGLLIEWHA  
15 YLFSMPILKDKEILRSTARLIVSDLMQFKITVFAGGGMLGALIYKPIAFLFSNIG  
AYMIGVLFILGLFLMSSLEVYDIVEFIRAFKNKVAEKHEQNKKERFAKREMK  
KAIAEQERIERQKAEEEAYLASVNNDPETGEILEDQAEDNLDDALPPEVSETST  
PVFEPEILAYETSPQNDPLPVEPTIYLEDYDSPIPNMRENDEEMVYDLDDVDVDD  
SDIENVDFTPKTTLVYKLPTIDLFAPDKPKNQSKEKDLVRKNIRVLEETFRSFGI  
20 DVKVERAEIGPSVTKEYEIKPAVGVRVNRISNLSDDLALALAAKDVRIEAPIPGK  
SLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSFNLARMPH  
LLVAGSTGSGKSVAVNGIISILMKARPDQVKFMMIDPKMVELSVYNDIPHLLI  
PVVTNPRKASKALQKVVDENRYELFSKIGVRNIAGYNTKVEEFNASSEKQ  
QMPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPSVD  
25 VISGLIKANVPSRIAFAVSSGTDSTRILDENGAEKLLGRGDMLFKPIDENHPVRL  
QGSFISDDDVERIVGFIKDQAEADYDDAFDPGEVSETDNGSGGGGGVPESDPL  
FEEAKGLVLETQKASASMIQRRLSVGFNRATRLMEELEAAGVIGPAEGTKPRK  
VLMTPTPSE\*

30

Sequence description:

35 A] Length: 2451 bp - 817 aa (Full-length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
peptide

40 ID-104

Clone 2-18/22b

(SEQ ID NO: 57)

ATGTCACAAGAGCAAGGAAAAATTTATATTGTAGAAGATGATATGACGAT  
TGTGTCACTTTTAAAAGATCATTTATCAGCTAGCTATCATGTCTCTAGTGTC  
AGCAATTTTCGTGATGTGAAACAAGAAATTATCGCATTTCAACCCGATTTG  
5 AACTAATGGATATTACGTTACCCTATTTTAATGGTTTTTACTGGACTGCAG  
AATTGCGTAAGTTTTTAACAATTCCTATTATTTTCATTTTCATCTAGTAATGA  
TGAAATGGATATGGTTATGGCATTAAATATGGGGGGTGATGACTTTATTTC  
AAAACCATTCTCTCTAGCTGTATTAGATGCTAAGCTAACTGCTATTTTAAG  
GAGAAGTCAACAATTTATCCAACAGGAATTAACTTTTGGGGGATTTACGTT  
10 GACAAGAGAAGGGTTATTGTCTAGCCAAGATAAAGAGGTTATTTTATCGC  
CAACAGAAAATAAAATCCTATCTATCTTGCTCATGCATCCTAAACAAGTAG  
TCTCAAAAGAGTCTCTATTAGAGAACTTTGGGAAAATGATAGTTTTATTG  
ATCAAAATACACTTAATGTTAATATGACACGCTTACGTAAAAAAATTGTCC  
CAATAGGTTTTGATTACATTCATACAGTGAGAGGAGTTGGGTATTTACTAC  
AATGA

15

(SEQ ID NO: 58)

MSQEQGKIYIVEDDMTIVSLLKDHLASYSYHVSSVSNFRDVKQEIIAFQPDILM  
DITLPYFNGFYWTAELRKFLTPIIFISSNDEMMDMVMALNMGGDDFISKPFSLA  
VLDAKLTAILRRSQQFIQQLTFGGFTLTREGLLSSQDKEVILSPTENKILSILLM  
20 HPKQVVSKESSLLEKLWENDSFIDQNTLVNMTRLRKKIVPIGFDYIHTVRGVG  
YLLQ\*

25 Sequence description:

25

A) Length: 669 bp - 223 aa (full-length gene  
sequence)

30 B) Shine Dalgarno sequence present upstream of a GTG start codon.  
Was not identified directly by LEEP. This gene was found upstream of  
gene ID-10 described in WO 00/06736.

ID-105

35 Clone 2-20

(SEQ ID NO: 59)

ATGTATCAAACCTCAGACAAATAAGGAAAAATTTGTTTTATTTTTGAAATTA  
40 TTTATCCCAGTATTGATTTATCAATTTGCTAATTTTTCAGCTACTTTTATTGA  
TTCGGTTATGACTGGACAGTATAGTCAGCTACATTTGGCAGGTGTGTCAAC  
TGCTAGTAATTTATGGACTCCGTTTTTCGCTTTATTAGTAGGTATGATTTCA  
GCATTAGTACCAGTAGTTGGTCAACATTTGGGTAGAGGAAATAAAGAACA  
AATTTCGCACAGAATTTTCATCAATTTCTATATTTAGGTTTGATACTGTCCTTA  
ATATTATTTTAAATCATGCAATTTATTGCTCAACCTGTCTTGGGGAGTTTGG

5 GTTTAGAAGATGAAGTTCTAGCAGTTGGTCGTGGTTATTTAAATTATATGT  
 TGATTGGAATCATGCCGCTGGTGTGTTTAGCATTGCGGTTCAATCCTTGA  
 TGCATTGGGGTTAACAAGGTATCTATGTATCTGATGCTTTTAATTCTACCC  
 TTTAATTCATTTTTTAATTATATGCTTATCTACGGTAAATTTGGTATGCCTA  
 10 GACTAGGAGGTGCGGGGGCAGGTCTTGGAACCTCTTTAACTTATTGGGCTA  
 TTTTATTGGTATTATTATTGTGATGTCACCTTCATCCTCAAATTAACACATA  
 TCATATATGGACTCTGGAAAGAATAAAAGCTCCTTTGATTATTGAAGATAT  
 TCGATTGGGATTACCGATTGGTTTACAAATTTTTGCAGAAGTTGCAATTTTT  
 GCAGTAGTAGGCTTATTCATGGCAAAATTTTCTTCAATCATTATTGCAGCA  
 15 CATCAGGCTGCTATGAATTTTTCATCATTAAATGTATGCATTTCTTTAAGTA  
 TTTCCACTGCTCTAGCTATTACAATATCGTTTGAAGTAGGGGCAGAGCGCT  
 TTCAGGACGCAACCACTTATAGTAGGATAGGACGCTTAACAGCGGTAGGG  
 ATTACATCAGGAACCTTACTATTTTTATTTCTATTTCTGTGAGAATGTAGCAG  
 CAATGTATAATAGTGCCCTCACCTTTGTCGCTATTACAGCTCAATTCCTAAC  
 20 TTATAGTCTCTTTTTCCAGTTTGCAGATGCTTATGCAGCTCCTGTACAGGGG  
 ATTTTACGAGGCTATAAGGATACAACAAAACCATTTATGATCGGTGCGGG  
 CTCTTATTGGTTATGTGCTTTGCCATTAGCGGTTATCTTAGAAAAAATAG  
 CCAGTTAGGTCCGTTTGCCTATTGGATTGGTTTAATCACAGGTATTTTTGTT  
 TGTGGTCTATTTCTAAACCAACGTCTGCAAAAGATTAAGAAGTTGTATTAT  
 TAA

(SEQ ID NO: 60)  
 MYQTQTNKEKFVLFLKLFIPVLIYQFANFSATFIDSVMTGQYSQLHLAGVSTAS  
 NLWTPPFALLVGMISALVPVVGQHLGRGNKEQIRTEFHQFLYLGLLSLILFLI  
 25 MQFIAQPVLGSLGLEDEVLA VGRGYLNYMLIGIMPLVLFISICRSFFDALGLTRL  
 SMYLMILLIPFNSFFNYMLIYGKFGMPRLGGAGAGLGTSLTYWAIFIGIIVMS  
 LHPQIKTYHIWTLERIKAPLIIEDIRLGLPIGLQIFAEVAIFAVVGLFMAKFSSIIA  
 AHQAAMNFFSLMYAFPLSISTALAITISFEVGAERFQDATTYSRIGRLTAVGITS  
 GTLLFLFLFRENVAAAMYN SAPHFVAITAQFLTYSLFFQFADAYAAPVQGILRG  
 30 YKDTTKPFMIGAGSYWLCALPLAVILEKNSQLGPFAYWIGLITGIFVCGLFLNQ  
 RLQKIKKLYY\*

35 Sequence description:

- A) Length: 1341 bp - 447 aa (full length gene)
- B) Shine-Dalgarno sequence present upstream of  
ATG start codon, There is a potential signal  
peptide sequence

40

ID-106

Clone 2-4A

(SEQ ID NO: 61)  
5 TTGCTAGTTTCTTCTCTAGTTTCTTGTTTCATTTTTTCTTGTCATTTTCGTCGTT  
GTCTTCATCAACACGAAATAAGTCTATAAACTTATCAAATAATTTTCATAGA  
CTTATTATATCAATTTTCAATAAAATGCTATAATAAAACCATGTCATTTTCA  
TTAAAAATTAGAAATCCATACGGTGAACATAACCGTTAAAGAACTCCTTGA  
10 AGATTATTTTTTTGATTCCACGTAAGATTAGACATTTTTTTCGCTGTTAAAAAA  
CATGTACTTATAAACAATGAATTCATTAATTGGCAAACCTGTCGTCCAAGAA  
AACGATACTATTACCTTAATCTTTGATGATGAGGATTACCCTACTAAAAAA  
ATTCCTCTGGGCAGAGCAGAGCTTATTGATTGTCTTTATGAGGATGAACAT  
CTTATTATCGTTAATAAACCTGAAGGTATGAAAACCTCACGGTAACCAACCA  
15 AATGAAATAGCACTGTTAAATCATGTATCTGCCTATTCTGGACAAACATGC  
TATGTTGTTTCATCGCCTAGATATGGAGACCAAGTGGAGCTGTTTTATTTGCT  
AAAAATCCATTTATACTTCCCCTTATCAATCAACGCTTAGAACGAAAAGAA  
ATTTGGCGTGAATATTGGGCTTTAGTTGAAGGAAAATTTTCACCTAAGCAT  
CAAGTTTTTGAGAGACAAAATTGGACGGAACCGTCATGACAGACGTAAACG  
AATCATTGATTCTAAAAACGGTCAACATGCTATGACAATCATTGACGTTTT  
20 GAAGTATATCCAAAATAGTAGTCTCATAAAATGCCGACTGGAAACCGGAA  
GAACCCATCAAATTCGCATTCACTTATCTCATCACGGACATCCTTTAATAG  
GAGATCCCCTCTACAACCCTTCTTCTAATAATGAAAGGTTAATGCTACACG  
CTCACCGATTGACTCTATCCCATCCATTAACCTTGCGAAACTATTAGCGTAG  
AGGCCCTTCATCTACTTTTCGAGAAGGTTTTAAACAATTATAAAAAAGGAG  
25 TTGGATAA  
(SEQ ID NO: 62)  
MLVSSLVSCSFFLVISSLSSSTRNKSINLSNNFIDLLYQFSIKCYNKTMSFSLKIR  
NPYGEHTVKELLEDYFLIPRKIRHFLRVKKHVLINNEFINWQTVVQENDTITLIF  
30 DDEDYPTKKIPLGRAELIDCLYEDEHLIIVNKPEGMKTHGNQPNEIALLNHVSA  
YSGQTCYVVHRLDMETSGAVLFAKNPFILPLINQRLERKEIWREYWALVEGKF  
SPKHQVLRDKIGRNRHRRKRIIDSKNGQHAMTIIDVLKYIQNSSLIKCRLETG  
RTHQIRIHLSSHGHPLIGDPLYNPSSNNERLMLHAHRLTLSHPLTCETISVEAPS  
STFEKVLNNYKKGVG\*

35

Sequence description:

- 40 A] Length: 1029 bp - 343 aa (Full length gene sequence)  
B] No obvious Shine-Dalgarno sequence upstream  
of the putative TTG start codon. Possesses a  
potential leader peptide sequence.

ID-107

Clone 2-54

5

(SEQ ID NO: 63)

GAAGTAAATGCAACTCAACCTAATAATAGAACTACCTATATTATACCCGAA  
AGCAGTCATTCCATTGCAGAACAACAGAGATTCCTGATAGAATCAAAGGG  
TTCTTCGGTTGCATTACTTAATAGCGATGAATTTAGAAAGACAGCGGGAGA  
10 GGATAGAGGTTTTGAAAGGGATAAGTTGAGGTCTTTGGATATCATTCTAA  
GGGAGATTTATCGACAAGTAATGTCATAGGTAATACGGACATTGCTAGTC  
AGATATCGTTGGGCTTTAAAAAGAATGCGATGCAGGAACACCATCTTACT  
AAAACATTCTCTCAAAGGATGGAAAGTTATCGTCTGTTATAGAGGGGAT  
GCTTGCTATTGGCAAAGAGAGAAAGTAGAGAAAGAAATAAAATATAGTGGTA  
15 ATTTATGGCAAAAATTAAGCTAAGGCACACTGCCTTGTTTGCTGTGTG  
ATAATTTGAATTTTGAAGATATAAAATCTTATTTTCAATATTATTGTCATCT  
AAACCATCAGCTCAAATTACCTAAAGGTGCTATACTTTCTGCTAAAACAGA  
AGTATATAGGGGAGGAGATTTTGGGAGAAAAAATAAAGATAATGTGTTTG  
GTTACCGTATCCCCCTCATTATTGAAAACCCAAAAAGGAACCTTACTTGCGG  
20 GAGCTGATGAAAGAATTGAGCAAGCTTGTGATTGGGGAAACATAGGAATG  
GTTATTCGCCGTAGTGAGGATGATGGTGTCACTTGGGGAAAAAGAGAAAC  
TATTGTCAATCTCCGTAATAACCCTAGAGTTCCGCTAGTTACTAGTGGTGA  
CTATAGTGGCTCACCTATTAATATGGATATGGCATTAGTTCAAGATACTAG  
CTCCAAGACGAAACGTATTTTTTCAATATATGATATGTTTCCAGAAGGAAG  
25 AGGCGTTATTAGTATTGCTAACACACCTGAAAAAGAATATACCCAAATCG  
GAGGACAGTCTTATCTTAATTTATATAATAATGGAAAGAAATCGAAGGTTT  
TACTATCCGTGACAAAGGTATTGTATATAATTTTAAAGGGAAAAAGACTG  
ATTATCATGTTATAACAGAACTACTAAAAGTGACCATTCAAATCTAGGGG  
ATATTTATAAGGGAAAAACAGCTACTTGGAAATATATATTTTACAAAACATA  
30 AAACGTCACCATTTTCGTTTAGCAAAATCAAGCTATGTGTGGATGTCATATA  
GCGATGATGATGGTAGGACATGGTCATCACCTAGAGATATAACAGCAAGT  
CTTCGTCAGAAAGGCATGAAATTTTTGGGAATAGGACCTGGAAAAGGTAT  
AGTTTTAAATGGGGGCCACACGCTGGTTCGTATTATTATTCCTGCCTATTCT  
ACGAATTGGAAATCTCATCTAAGAGGTTTACAATCTTCACGCCTAATTTAT  
35 TCAGACGACCATGGAAAAACGTGGCATACTGGAAAAGCAGTTAATGATAA  
CCGTATACTTTCTAATGGTGAAAAAATTCACCTCCTTAACAATGGATAATAA  
AAAAGAACAAAATACAGAATCCGTACCCGTTCAATTGAAAAATGGGGACA  
TTAAGTTATTTATGAGGAATCTAACTGGTAACCTAGAAGTAGCCACAAGTA  
AAGACGGCGGGGAGACTTGGCAAAACCATGTTAAACGATATAAGGAAATT  
40 CATGATGCTTACGTCCAACCTATCAGCTATTTCGCTTTGAGCATGACAAAAA  
GAGTATATTTTATTAGTGAATGCTAATGGGCCAGGGAAGAAGTGCCAAGA  
TGGATATGCACGTCTAGCGCAAGTTAATCGAAATGGTAGTTTAAAGTGGTT  
ATATCACCATCACATTCAAGATGGTTCGTTTGCTTACAACCTCTGTTCAACA  
ACTTAATAATGATCAATTTGGTGTCTTTTATGAACATAGAGAAAAACATCA

AAATAGTTTTACTTTAAATTACAAAGTTTTTAATTGGAGTTTTCTTAGTCAA  
AATACAGAGAAGCAAGGCACTTTATGGGAGAAAATGGCAGCAAATTGGCA  
TGTTTTGTTTAAATTTTATTTATGA

5

(SEQ ID NO: 64)

ELNATQPNNRRTTYIPESSHSIAEQQRFLIESKGSSVALLNSDEFKRTAGEDRGF  
ERDKLRSLDIIPKGDLSNSVIGNTDIASQISLGFKKNAMQEHLTKTFSQKDG  
KLSSVIEGMLAIGKEKVEKEIKYSGNLWQKLKAKAHCLVCCVDNLNFEDIKS  
YFQYYCHLNHQLKLPKGAILSaktevyrGGDFGRKNKDNVFGYRIPSLKKTQ  
10 KGTLLAGADERIEQACDWGNIGMVIRSEDDGVTWGKRETIVNLRNNPRVPL  
VTSGDYSGSPINMDMALVQDTSSSKTKRIFSIYDMFPEGRGVISIANPEKEYTQI  
GGQSYLNLYNNGKKSUVFTIRDKGIVYNFKGKKTDYHVITETTKSDHSNLGDI  
YKKGQLLGNIYFTKHKTSPFRLAKSSYVWMSYSDDDGRTWSSPRDITASLRQ  
KGMKFLGIGPGKGIVLKWGPHAGRIIPAYSTNWKSHLRGSQSSRLIYSDDHG  
15 KTWHTGKAVNDNRILSNGEKIHSITMDNKKKEQNTESVPVQLKNGDIKLFMRN  
LTGNLEVATSKDGGGETWQNHVKRYKEIHDAYVQLSAIRFEHDKKEYILLVNA  
NGPGKKCQDGYARLAQVNRNGSFKWLYHHHIQDGSFAYNVQQLNNDQFG  
VLYEHREKHQNSFTLNYKVFNWSFLSQNTTEKQGTLEWMAANWHVLFKFYL  
\*

20

Sequence description:

A] Length: 2052 bp - 684 aa (partial gene sequence)

B] N-terminus has yet to be determined

25

ID-108

30

Clone 2-61

(SEQ ID NO: 65)

ATGCCTAAATTAATCGTATCTTTCCTCTGCATTTTATTATCCCTGACTTGTG  
TAAACTCTGTGCAAGCTGAAGAACATAAAGATATTATGCAAATTACCCGA  
35 GAAGCCGGATATGATGTAAAGATATTAATAAACCTAAAGCGTCTATCGTT  
ATTGACAATAAAGGTCATATTTTGTGGGAAGATAACGCCGATTTAGAACGT  
GATCCCGCTAGCATGTCTAAAATGTTTACTTTATATTTACTATTTGAAGACT  
TAGCTAAAGGAAAAACAAACCTCAACACCACAGTGACTGCAACAGAAACA  
GACCAAGCCATAAGTAAGATTTATGAAATTAGTAATAACAATATTEATGCT  
40 GGGGTTGCTTATCCTATTCGTGAACTGATTACTATGACGGCTGTCCCGTCA  
TCTAATGTAGCAACTATTATGATTGCTAACCACTTATCACAAAACAATCCT  
GACGCCTTTATTAAACGAATCAATGAAACCGCCAAGAACTCGGTATGAC  
AAAAACTCACTTTTATAACCCAGTGGGGCGGTAGCGAGTGCTTTTAATGG  
ACTTTACTCCCCAAAAGAATACGATAACAATGCTACTAACGTTACGACTGC



ACGTGATCTATCAATTTTAACCTATCATTTTCCTTAAAAAATACCCTGATATA  
CTGAACTATACAAAATATCCTGAAGTCAAGGCCATGGTCGGAACCTCCTTAT  
GAAGAAACATTTACAACCTTATAACTACTCTACCCCCGGCGCTAAATTTGGA  
TTAGAAGGAGTAGATGGCTTAAAAACTGGTTCTAGCCCTAGCGCTGCTTTT  
5 AATGCCTTAGTTACAGCTAAACGCCAGAATACTCGCTTGATAACTGTGGTT  
TTAGGAGTTGGCGATTGGTCAGACCAAGACGGAGAGTACTATCGTCATCC  
GTTTGTCAACGCTCTTGTAGAAAAAGGTTTTAAAGACGCTAAAAATATTTC  
TTCTAAAACTCCTGTATTAAGCCGTTAAACCTAAAAAAGAAGTTACTAA  
AACCAAAACCTAAATCTATTCAAGAACAGCCTCAAACAAAAGAACAGTGGT  
10 GGACAAAACAGATCAATTTATCCAATCACATTTTGTATCTATTTTAATTG  
TTCTGGGCACCATCGCTAGCCTTTGTCTTTTAGCTGGGATAGTATTACTTAT  
AAAGCGCTCTAGATAA

(SEQ ID NO: 66)  
15 MPKLIVSFLCILLSLTCVNSVQAEHKDIMQITREAGYDVKDINKPKASIVIDN  
KGHILWEDNADLERDPASMSKMFTLYLLFEDLAKGKTNLNTTVTATETDQAI  
SKIYEISNNNIHAGVAYPERELITMTAVPSSNVATIMIANHLSQNNPDFAIKRINE  
TAKKLGMTKTHFYNP SGAVASAFNGLYSPKEYDNNATNVTTARDLSILTYHF  
LKKYPDILNYTKYPEVKAMVGTPEETFTTYNYSTPGAKFGLEGVDGLKTGS  
SPSAAFNALVTAKRQNTRLITVVLGVGDWSDQDGEYYRHPFVNALVEKGFK  
20 DAKNISSKTPVLKAVKPKKEVTKTKTKSIQEQPQTKEQWWTKTDQFIQSHFVS  
ILIVLGTIASLCLLAGIVLLIKRSR\*

25 Sequence description:

A] Length: 1188 bp - 396 aa (full length gene)  
B] Shine Dalgarno sequence present upstream of  
ATG start codon, possesses a potential signal  
30 peptide

35 ID-109

Clone 45

(SEQ ID NO: 67)  
40 ATGACTGAAAAATATTATAATTGGGCAACGCTTGGAACCGGCGTTATTGCC  
AACGAATTAGCCCAAGCACTGGAAGCACGTGGACAAAAATTATATTCTGT  
AGCTAATAGAACTTACGACAAAGGACTTGAATTTGCTAACAAATATGGTA  
TCCAAAAAGTTTATGATCACATAGATCAAGTATTTGAAGACCCTGAAGTGG  
ATATCATTTATATCTCTACTCCCCACAATACTCACATCTCATTTTTACGAAA

GGCTTTAGCAAATGGTAAGCACGTTCTTTGCGAAAAATCTATTACTTTAAA  
TAGTACTGAGCTTAAAGAAGCCATAGATTTAGCCGAAACTAACCATGTTGT  
CTTAGCTGAAGCCATGACTATTTTTCATATGCCAATTTACCGCCAATTTAAA  
AACATTAGTTGATAGTGGAAAATTAGGACCGTTAAAAATGATTCAAATGA  
5 ATTTTCGGAAGTTATAAAGAATATGATATGACTAACCGTTTTTTCAGTCGTG  
ACCTAGCAGGCGGTGCTTTGCTGGACATTGGTGTGTTATGCACTTTCTTGTAT  
TCGCTGGTTTATGTCAGAAGCACCTCACAACATTACCTCTCAAGTTACATT  
TGCACCAACAGGGGTTGATGAACAAGTTGGTATCCTACTAACCAACCCAG  
CAAATGAGATGGCGACTGTCAGCCTTAGTTTACATGCAAAACAACCTAAA  
10 CGAGCAACTATCGCTTACGATAAAGGCTACATTGAACTTTTTGAATATCCG  
CGAGGACAAAAGGCAGTTATTACTTATACTGAGGATGGGCATCAAGATAT  
TATCGAAGCTGGCAAAACTGAAAATGCTCTCCAATATGAGGTAGCTGATA  
TGGAAGAAGCCATTTTCAGGAAAAACTAACCACATGTACTTAAACTATACC  
AAAGATGTTATGGATATCATGACACAGCTACGTCAAGAATGGGGATTTAC  
15 CTACCCAGAAGAAGAAAAATGA

(SEQ ID NO: 68)  
MTEKYYNWATLGTGVIANELAQALEARGQKLYSVANRTYDKGLEFANKYGI  
QKVYDHIDQVFEDPEVDIIYISTPHNTHISFLRKALANGKHVLCESITLNSTEL  
KEAIDLAETNHVVLAEAMTIFHMPYRQLKTLVDSGKLGPLKMIQMNFGSYK  
20 EYDMTNRRFFSRDLAGGALLDIGVYALSCIRWFMSEAPHNITSQVTFAPTGVDE  
QVGILLTNPANEMATVSLSLHAKQPKRATIAYDKGYIELFEYPRGQKAVITYT  
EDGHQDIIEAGKTENALQYEVADMEEAISGKTNHMYLNYTKDVMDIMTQLR  
QEWGFTYPEEEK\*

25 Sequence description:

A] Length: 984 bp - 328 aa (full length gene)  
B] Shine Dalgarno sequence present upstream of  
30 ATG start codon, possesses a potential signal  
peptide

35 ID-110

Clone 2-2

40 (SEQ ID NO: 69)  
GTGTATTCTCCTGTAAATCTTCTAAAGGAAAAGTGATATTGTAAAAAGT  
GATTTTCTAAAGAGCTTCATAGAAAGGAGAGGAAATATTTGTTTT  
(SEQ ID NO: 70)  
MYSPVKSSKGVILLKSDFLKSFIERGNICF

Sequence description:

5                   A] Length: 96 bp - 32 aa (partial sequence)  
                  B] GTG start codon - no obvious Shine-Dalgarno  
                  sequence  
                  Possesses a potential signal peptide

10

ID-111

15               Clone 2-3

(SEQ ID NO: 71)  
AAATACTGTATCATTGCAACCTCAAATGCAGGTTTTGGAAACGAAGCATTT  
ACAGGTGACAGCGATAAAGACTTGAAAATTATGGAACGAATTTCTCCATA  
20               TTCCGTC CAGAATTTCTAAATCGTTTCAATGGTGTTATTGAATTCTCTCAC  
                 CTAAGCAAAGATGACTTAAGCGAAATTGTAGATTTGATGCTTGATGAAGTT  
                 AACCAAACAATTGGCAAAAAAGGAATTGACCTTGTGGTAGATGAAAATGT  
                 TAAATCACACTTAATTGAACTGGGTTATGACGAAGCAATGGGAGTACGTC  
                 CATTGCGCCGTGTCATCGAGCAAGAAATTCGAGATCGCATCACAGACTACT  
25               ATCTCGATCATAACAGACGTTAAACACCTAAAAGCTAATTTGCAAGATGGCC  
                 AAATCGTCATTTCTGAAAGATAA  
                 (SEQ ID NO: 72)  
                 KYCIIATSNAGFGNEAFTGDSKDLKIMERISPYFRPEFLNRFNGVIEFSHLSKD  
                 DLSEIVDLMLDEVNQTIGKKGIDL VVDENVKSHLIELGYDEAMGVRPLRRVIE  
30               QEIRDRTDYLDHTDVKHLKANLQDGGQIVISER\*

Sequence description:

35                   A] Length: 429 bp - 143 aa (partial sequence)  
                  B] N-terminus yet to be elucidated. This gene  
                  was not in frame with nuc

40

ID-112

Clone 2-5

(SEQ ID NO: 73)

ATGTCAATGAATTTTTCATTTTACCACAATATTGGTCCTATTTTAATTATG  
GTGTGATGGTAACCATTATGATTTCAACATGTGTTGTTTTTTTGGAACTAT  
TATAGGCGTGTTAATTGCTTTAGTAAAGCGTACTAATTTACATTTTCTCACA  
ATATTAGCTAATTTCTATGTATGGGTATTTTCGTGGGACACCGATGGTAGTT  
5 CAAATTATGATTGCTTTTCGCATGGATGCATTTTAACAATTTACCAACAATT  
AGCTTTGGTGTTTTAGATTTAGATTTTACACGACTTTTACCTGGTATCATT  
TCATTTCTTAAATAGTGGTGCCTATATTTTCGGAAATTGTACGTGCAGGGA  
TTGAGGCTGTACCATCTGGACAAATAGAAGCAGCTTACTCGTTGGGGATT  
GACCTAAAAATACACTTCGCTATGTTATCTTACCCCAAGCTTTTAAAAATA  
10 TTTTACCTGCTCTAGGGAATGAATTTATTACAATTATTAAAGATAGTGCTCT  
CCTTCAAACCTATTGGTGTCATGGAATTATGGAACGGAGCACAATCAGTTGT  
AACGGCTACTTACTCACCAGTTGCACCGTTATTATTTGCAGCATTTTACTAT  
TTAATGTTGACAACGATTCTCTCAGCTTTGTTAAAACAAATGGAGAAATAT  
CTTGGGAAAGGGGTAAAAATAGATGGTTGA

(SEQ ID NO: 74)

MSMNFSFLPQYWSYFNYGVMVTIMISTCVVFFGTIIGVLIALVKRTNLHFLTIL  
ANFYVWVFRGTPMVVQIMIAFAWMHFNNLPTISFGVLDLDFTRLLPGIIISLNS  
GAYISEIVRAGIEAVPSGQIEAAYSLGIRPKNTLRYVILPQAFKNILPALGNEFITI  
IKDSALLQTIGVMELWNGAQSVVTATYSPVAPLLFAAFYYLMLTTILSALLKQ  
20 MEKYLKGKGVKIDG\*

Sequence description:

25 A] Length: 699 bp - 233 aa (full length gene)  
B] Shine-Dalgarno sequence preceded the 'ATG'  
start codon. Possesses a potential leader peptide  
sequence.

30

ID-113

35 Clone 2-7

(SEQ ID NO: 75)

ATGAAAGACCTATTACGAAATAGTCTAGAGCAAAGTGGAAATTTAAGTTT  
TCAAGATATGATTTTACATATTCTTGTAGCAGCTTTATTGAGTGTAGTTATT  
40 TATGTTTCCTATGCTTATACGCATAGTGGAACTGCCTATAGTAAAAAGTTT  
AATGTTTCATTAATGACATTGACGGTCTTGACTGCAACAGTAATGACCGTT  
ATTGGTAATAATGTAGCCTTGTCATTGGGTATGGTCGGTGCCTTGTCAGTT  
GTTTCGTTTTAGGACAGCCATAAAAGATTCAAGAGATACAGTTTATATTTT  
TGGACCATAGTTGTTGGTATCTGTTGTGGTGTCTGGTGACTATGTGGTAGCT

GCATTAGGAAGTAGCGTTATCTTTATCTTATTATGGGTTATGGGACGTGTT  
AAAAACGAGAATCGTATGTTATTGATTGTGAAGTGCGATAGAACTAGA  
AGTTGATTTAGAAGGAATTTTCTTCCAATATTTTGACGGAAAAGCTGTTCA  
GCGTGTTAAAAATTCAACAATACTATTGAAATGATTTTCGAAATCTC  
5 TAGAAAAGATTACGATAAGCAACTCCATGTAGATAATCAGTTAACTGAAA  
AAGTGTACCAATTGGGAAATATTGATTATTTCAACATTGTTAGCCAAAGCG  
ACGAAATCAATGGGTAG

(SEQ ID NO: 76)  
MKDLLRNSLEQSGNLSFQDMILHILVAALLSVVIYVSYAYTHSGTAYSKKENV  
10 SLMTLTVLTATVMTVIGNNVALSLGMVGALS VVRFRRTAIKDSRDTVYIFWTIV  
VGICCGVGDYVVAALGSSVIFILLWVMGRVKNENRMLLIVKCDRTLEVDLEGI  
FFQYFDGKAVQRVKNSTTNTIEMIFEISRKYDYDKQLHVDNQLTEKVYQLGNID  
YFNIVSQSDEING\*

15  
Sequence description:

A] Length: 678 bp - 226 aa (full-length gene)  
B] ATG start codon is preceded by a Shine-  
20 Dalgarno sequence-Possesses a potential leader  
peptide sequence

25 ID-114

Clone 2-8

(SEQ ID NO: 77)  
30 AAAAATTCATTTTAGATTCATTTTACGACTATATACTCAGAAGTACCAAAC  
CTAATCCAAGGTTTGAAAAAAGAAAGAAGGAAGTCAGTATGACAACTAT  
AAAAACAACTTTAAAGATGAGGCTATACGTGTTGAAGAGACAACAAAAGA  
ATCATTTTACGATGTTGATATTGCCTTGTTTTTCAGCTGGTGGATCTATTTCA  
GCAAAGTTCGCTCCTTATGCAGTAAAGTCTGGAGCAGTTGTAGTAGATAAC  
35 ACGTCATATTTTCGTCAGAAATCCTGATGTTCCACTAGTTGTTCCCTGAAGTAA  
ATGCTCATGCCATGATTGGTCATAATGGTATCATAGCTTGTCCTCAATTGTTT  
TACTATTCAAATGATGATTGCTTTAGAGCCCATTCGTCAAAAATGGGGGAT  
AGAGCGTGTTATAGTTTCCACCTATCAAGCTGTTTCGGGTTTCAGGTGCACG  
TGCTGTTGAAGAACTAAGGAACAGTTGAGACAAGTTT

40 (SEQ ID NO: 78)  
KFILDSFYDYILRSTKPNPRFEKRKKEVSMTNYKNNFKDEAIRVEETTKESFYD  
VDIALFSAGGSISAKFAPYAVKSGAVVDNTSYFRQNPDPVPLVVPEVNAHAMI  
GHNGIACPNCTIQMMIALLEPIRQKWGIERVIVSTYQAVSGSGARAVEETKEQ  
LRQV

Sequence description:

- 5                   A] Length: 499 bp - 165 aa (partial sequence)  
                  B] N-terminus has yet to be determined

ID-115

10

Clone 2-9

15           (SEQ ID NO: 79)  
          ATGACAAATGAATTGATAATGCAAGCTTTTGAGTGGTATTTACCTAGTGAT  
          GGGAATCACTGGAAGAAATTAGAGGAGTCTATATCAGACCTTAAAAAACT  
          TGGAATTAGTAAAATCTGGTTACCACCAGCATTTAAGGGAACTAGCAGTG  
          ATGATGTAGGATATGGTGTTTATGATCTCTTTGATTTAGGAGAATTTGACC  
          AGAATGGAACAATTAGAACAAAATATGGTAGGAAAGAAGAGTATCTAAA  
20           GCTTATTAAGTCGTTAAAGGCAAATGGCATTAAACCGTTTGCAGATATCGT  
          TCTTAACCATAAAGCCAATGGTGATCATAAAGAAAAATTTCAAGTCATCA  
          AAGTCAATCCTGAAAATCGTCAAGAAGCATTAAAGTGAACCCTATGAGATT  
          GAAGGATGGACGGGATTTGATTTCCCAGGTAGACAGGGTGAGTACAATGA  
          TTTT  
25           (SEQ ID NO: 80)  
          MTNELIMQAFEWYLPDGNHWKKLEESISDLKKLGISKIWLPPAFKGTSSDDV  
          GYGVYDLFDLGEFDQNGTIRTKYGRKEEYKLIKSLKANGIKPFADIVLNHKA  
          NGDHKEKFQVIKVNPNENRQEALSEPYEIEGWTGFDFPGRQGEYNDF

30

Sequence description:

- A] Length: 456 bp - 152 aa (partial sequence)  
                  B] ATG start codon is preceded by a Shine-  
35               Dalgarno sequence, no leader peptide sequence.

ID-116

40

Clone 2-10

(SEQ ID NO: 81)

ATGGAGGTTCTTATGAAGAAAGTGTTAGTAAGTAGTCTTTTGGTTTTAGGG  
ATTACGATAACGTTACAACCAGTAGTTGAGGCTAAGGGGCCAAAAGTAGC  
TTATACACAAGAGGGAATGACTGCTCTTTCGGACACAAATAAAGATAAAG  
TCACTACTATTTCTATTGACGAGATTCAAAAAAGCTTAGAAGGTAAGAAGC  
5 CGATTACTGTTAGTTTTGATATTGATGATACACTGCTTTTCAGTAGTCAATA  
TTTTCAATATGGTAAAGAATATGTAACCTCCTGGATCGTTTGATTTTCTTCAT  
AAACAAAAAATTCTGGGATCTTGTTGCAAAACGAGGAGATCAAGATTCCAT  
TCCCAAAGAATATGCTAAAAAATTAATTGCTATGCATCAAAAACGAGGAG  
ATAAAATTGTTTTTATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAG  
10 GGCGAGGTTGATAAAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTTGTA  
CCATCTGAT

(SEQ ID NO: 82)

MEVLMKKVLVSSLLVLGITITLQPVVEAKGPKVAYTQEGMTALSDTNKDKVT  
TISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQYGKEYVTPGSFDFLHKQKFW  
15 DLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGSMYKEGEVDKTA  
KALAKDFKFVPSD

Sequence description:

20

A] Length: 516 bp - 172 aa (partial sequence)  
B] ATG start codon is preceded by a Shine-  
Dalgarno sequence, Possesses a leader peptide  
sequence.

25

ID-117

30

Clone 2-17

(SEQ ID NO: 83)

ATGCTTAAAAGATTATTTACTGAAGATGGGGAATTGACAAAGATTAGTCGT  
CGTTTCGTTTGGATGTTAGTGGTTATCTATTGTCTTATTATTGTCAGGATGT  
35 GTTTTGGGCCTCAAATTATGATTGAGGGGGTATCAACTCCGAATGTTTCAGC  
GCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTTAATTCTTTTCGTAGTTT  
AGATCAGCTAACTAGCTTTAAAGAGATTCTTTGGGTTATTGGTCAAAATGT  
AGTGAATATTTTACTGCTGTTTCCTCTCATTATAGGGTACTATCCCTAAAG  
CCAAGTTTACGGAAATATAAAAGCGTTATATTACTTGETTTCTTGATGTCTC  
40 TTTTCATAGAGTGTACTCAAGTTGTTTTAGATATTTTAATAGATGCTAATCG  
GGTTTTTGAAATCGACGATCTATGGACAAATACCTTAGGCGGTCCTTTTCGC  
CCTATGGAGTTATCGAAACATAAAAGGTTGGCTTCTAACTATTAGAAAATG  
A

(SEQ ID NO: 84)

MLKRLFTEDGELTKISRRFVWMLVVIYCLIIVRMCFGPQIMIEGVSTPNVQRFG  
RIVALLVPFNSFRSLDQLTSFKEILWVIGQNVVNILLFPLIIGLLSLKPSLRKYK  
SVILLAFLMSLFIECTQVVLDILIDANRVFEIDDLWTNTLGGPFALWSYRNIKG  
WLLTIRK\*

5

Sequence description:

- 10           A] Length: 516 bp - 172 aa (full-length gene)  
              B] ATG start codon is preceded by an Shine-  
                  Dalgarno sequence. Possesses a potential leader  
                  peptide sequence. C-terminus need further  
                  confirmation.

15

ID-118

20           Clone 3-3

20

(SEQ ID NO: 85)

ATGAAAAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTTCG  
TATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA  
ATATTTGATAAAGAATTAATCCATGAATATATTTTACAGGAATCAGTGGGG  
25           CAATTATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAACT  
              GAAAGCATATTTTACAAAAGAACAAGAAAGTCGAGATTCTAAAATACATT  
              TAATGCCATATGCAAAGAGATTTTAGAATGGACCAAAGAACAAGATATT  
              CCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGTGTGGAA  
              ACCTTGCAGATCTCTCATTATTTTGATGAAATTTTAACTGGTGTTCGGGAT  
30           TCGAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAAACGATATT  
              CTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGG  
              AGGTTGCTCAAAATGCTGGTATAAAATCCATAAACTTAAGGTTAGAGAATT  
              CCAAAGAAAACCTATAATATTTCAAGTCTCAAAGATATAATCACTTGATT  
              TCACTCGTTTGGATTAA

35

(SEQ ID NO: 86)

MKKLTFIWDLTGTLIDSYPIMEALEETYRHFGLIFDKELIHEYILQESVGQLL  
VNLSEEEQIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYYH  
KGASTHSVLETLQISHYFDEILTGVS GFERKPHPQGINYLVKRYSLDKSMTYYI  
GDRPLDLEVAQNAGIKSINLRLNSKENYNISLKDIIISLDFTRLD\*

40

Sequence description:

- A] Length: 627 bp - 209 aa (Possible Full-length gene)



B] ATG start codon is preceded by an possible  
Shine-Dalgarno sequence. No obvious leader  
peptide sequence.

5

ID-119

Clone 3-7

10

(SEQ ID NO: 87)

ATGGAAAAAGAAAAAAATTAGGTCTTTTACCACTAACAATGCTTGTCATT  
GGCTCTCTTATCGGTGGCGGAATCTTTGATTTAATGCAAAATATGAGTTCC  
AGAGCCGGTTTGGTACCAATGCTTATTGCTTGGGTAATTACTGCTATCGGG  
15 ATGGGAACTTTTCGTTTTAAGTTTTCAAAATTTATCTGAAAAAAGGCCGGAC  
CTAACAGCTGGAATCTTTAGTTACGCTAAAGAGGGGTTTGGAACTTTATG  
GGATTAACTCTGCATGGGGTTATTGGTTATCAGCTTGGCTTGGAAATGTT  
GCCTACGCTGCACTCTTATTCAGTTCACCTCGGTTATTTCTTTAAATTCTTTG  
GTAATGGAAATAATATCATCTCAATTATTGGAGCAAGTATAGTTATTTGGG  
20 TTGTCCATTTCTTAATTTTAAGAGGTGTTAATACAGCTGCATTTATTAATAC  
CGTAGTTACCTTTGCAAAATTAGTACCTGTTATTATTTTCTTAATTTTCAGCG  
TTATTAGCTTTCAAATTTAACATTTTTAGTCTTGATATCTGGGGAAATGGAT  
TACATCAATCAATTTTCAACCAAGTCAATTCAACTATGAAAACCGCTGTTT  
GGGTATTTATTGGTATTGAGGGCGCCGTTGTCTTCTCAGGTCGTGCTAAAA  
25 AACACTCTGATATTGGTAAAGCAAGTATCCTAGCATTATTCACCTATGATTT  
CACTTTATGTATTGATTTCTGTTTTATCACTTGGTATCATGTACAGTCCAGA  
ACTTGCAAACCTTAAAAACACCAGCTATGGCTTACGTTCTAGAAAAAGCTGT  
TGGTCACTGGGGTGCTATCTTAGTTAACCTTGGTGTTATCATTTTCAGTATTT  
GGCGCTATTCTTGCTTGGACTTTATTTGCAGCAGAATTACCATATCAAGCT  
30 GCTAAAGAAGGTGCTTTTCCTAAATTTTTTGCAAAAGAAAATAAAAAACAA  
AGCTCCAATCAACTCACTCTTAGTCACTAATCTTTGTGTACAAGCATTCTTA  
ATCACGTTCTTATTCACACAAAGTGCTTATCGTTTTGGTTTCGCATTAGCAT  
CATCTGCTATCTTAATTCCTTATGCTTTTACAGCACTATATCAATTACAATT  
CACACTCCGTGAGGATAAGTCAACTCCAGGACATCAAAAGAATTTAATTA  
35 TCGGTATCCTCGCTACAATCTATGCTGTTTACCTTATCTACGCTGGTGGTTT  
TGATTACTTACTTTTGACAATGATTGCTTATACTCTAGGTATGATTCTCTAT  
ATTAAAATGAGAAAAGATGACAAGCTTGGCGTAATCATGGTCATAGCTGT  
TTCCAGTGTGAAATTGTTATCC

40

(SEQ ID NO: 88)

MEKEKKLGLLPLTMLVIGSLIGGGIFDLMQNMSSRAGLVPMLIAWVITAIGMG  
TFVLFSQNLSEKRPDLTAGIFS YAKEGFGNFMGFNSAWGYWLSAWLGNVAY  
AALLFSSLGYFFKFFGNGNNIISIIGASIVIWVVHFLILRGVNTAAFINTVVF  
LVPVIIFLISALLAFKFNIFSLDIWGNGLHQSFNQVNSTMKTAVWVFIGIEGAV

5 VFSGRAKKHSDIGKASILALFTMISLYVLISVLSLGIMSRPELANLKTPAMAYV  
LEKAVGHWGAILVNLGVIIISVFGAILAWTLFAAELPYQAAKEGAFPKFFAKEN  
KNKAPINSLLVTNLCVQAFLITFLFTQSA YRFGFALASSAILIPYAFTALYQLQF  
TLREDKSTPGHQKNLIIGILATIYAVYLIYAGGFDYLLLT MIA YTLGMILYIKMR  
KDDKLG VIMVIAVSSVKLLS

Sequence description:

10

A] Length: 1356 bp - 452 aa (partial sequence)  
B] ATG start codon is preceded by an possible  
Shine-Dalgarno sequence. Possesses a potential  
leader peptide sequence.

15

ID-120

20

Clone 3-8

(SEQ ID NO: 89)  
25 ATGAAATTTGAAAAACGGCAGGTCTATTATGTTGTCATAACATTTGCTATT  
TGCTATGCTATACAGGCTTATTGGGGAGCTGTTTCTAATATTTTAACTACGC  
TTCATAAGGCAATATTTCTTTTTTGATGGGAGCTGGAATTGCCTATATTAT  
TAATATTGTAATGTCAGTCTATGAGCGATTATATATAAAGCTTTTTAAAGG  
ATCTAGACTATTAATGGCAATCAAGCGTAGTGTTTCTATGATTTTATCCTAT  
GCAACTTTTATTGGTTTAATTGTCTGGCTATTTTCAATTGTCATTCCAGATT  
30 TGATTTCTAGTTTGAGTTCTTTATTGGTTATTGATACCGGAGCACTTGCTAA  
ATTGGTTAATAATCTCAATGAAAATAAACA AATTTCTGAGGCTTTAAATTA  
TATGGGAACAGATAAAGACTTAGTTTCTACTTTAAGTGGTTATAGCCAGCA  
GATTTTGAAGCAAGTTTTATCTGTTTTAACA AATTTACTAACCTCAGTTTCC  
TCTATTGCGGCAACACTTCTGAATGTTTTTGTTAGTTTTATTTTTTCAATTTA  
35 CGTTTTGGCAAACAAGGAGCAGTTGGGACGTCAATTTAATTTGTTAATTGA  
TACCTATTTAGGTTCAACAGGCAAAACATTCCATTACGTTTCGTCATATCCTT  
CATCAACGTTTCCATGGTTTTTTTTGTAAGCCAAACTTTAGAAGCTATGATTT  
TAGGAAGTTTGACGGTTATTGGTATGTTGATCTTCCAATTTCCCTTATGCTTT  
AACAGTTGGGGTTTTAGTTGCTTTTACAGCTCTAATACCGGTTGTGGGAGC  
40 CTACATTGGTGTTACAATCGGTTTCATCTTAATTGCTACTGAATCGCTTACT  
GAAGCATTCTTGTTTGTTCTTTTCTTGATCCTTTTACAACAATTTGAGGGAA  
ATGTCATTTATCCGAAAGTTGTCTGGTGGATCGATTGGACTGCCTTCTATGT  
GGGTTTTAATGGCTATTACTATCGGAGGTGCTTTATGGGGGATCTTAGGCA

TGTTACTTGCTGTTCTGTTGCAGCTACTATCTATCAGATTGTAAAAGATCA  
TATTATCAAGCGACAAACGCTTAGAAATCGTGCACGAACCTATCGTTAA

(SEQ ID NO: 90)

5 MKFEKRQVYYVVITFAICYAIQAYWGAVSNILTLHKAIFPFLMGAGIAYINI  
VMSVYERLYIKLFKGSRLMAIKRSVSMILSYATFIGLIVWLFSIVIPDLISLSS  
LLVIDTGALAKLVNNLNENKQISEALNYMGTDKDLVSTLSGYSQQILKQVLSV  
LTNLLTSVSSIAATLLNVFVSFISYVLANKEQLGRQFNLLIDTYLGSTGKTFH  
YVRHILHQRFHGFFVSQTL EAMILGSLTVIGMLIFQFPYALTVGV LVAFTALIP  
10 VVGAYIGVTIGFILATESLTEAFLFVLFLILLQQFEGNVIYPKVVGGSIGLPSM  
WVLMAITIGGALWGILGMLLAVPVAATYIYQIVKDHIIKRQTLRNRARTYR\*

Sequence description:

15 A] Length: 1134 bp - 378 aa (full-length gene)  
B] ATG start codon is preceded by an typical  
Shine-Dalgarno sequence. Possesses a potential  
leader peptide sequence.

20

ID-121

Identical to ID-68, as described in WO 00/06736

25

ID-122

30

Clone 3-16

(SEQ ID NO: 91)

35 GTGATTACAATTAAAAAGGAATCTGTTATCAAACCTATTGAAGTATGCTTTT  
GGCATTATAATGGGATTTATTATCTTAGCTATTGTAATAGGTGGGCTCCTA  
TTTGCATACTACGTTAGTCGTTCTCCGAAATTAACCGATCAAGCTTTAAAA  
TCCGTTAACTCTAGTTTGGTTTATGATGGTAATAATAAACTTATTGCCGATT  
TAGGCTCAGAAAAGCGTGAAAGTGTTAGTGCGGATAGCATTCCACTAAAT  
TTGGTTAACGCTATCACTTCTATAGAAGATAAACGTTTCTTTAAACATAGA  
40 GGTGTCGATATTTATCGTATTTTAGGTGCAGCTTGGCATAACCTTGTTAGTA  
GTAATACGCAAGGTGGTTCAACCCTTGATCAACAGTTGATTAACTGGCTT  
ACTTTTCTACCAATAAATCTGACCAAACGTTAAAACGTAAATCACAGGAA  
GTTTGGCTTGCGCTTCAAATGGAGCGTAAATACACCAAAGAAGAAATTCTT  
ACTTTCTATATTAATAAAGTTTATATGGGAAATGGGAATTATGGTATGAGA

ACAACAGCTAAATCATACTTTGGTAAAGACCTAAAGGAATTATCTATTGCA  
CAACTTGCTTTGCTCGCTGGTATTCCTCAAGCACCTACACAATATGACCCTT  
ATAAAAACCCAGAATCTGCTCAAACAAGACGTAATACCGTTCTTCAGCAG  
ATGTATCAAGATAAAAACATTTCTAAAAAGGAATACGACCAAGCTGTTGC  
5 AACTCCAGTAACTGATGGCTTAAAAGAATTAAAGCAAAAATCTACTTATCC  
AAAATATATGGATAACTACTTAAAACAAGTTATTAGTGAAGTTAAACAAA  
AACTGGTAAAGATATCTTTACTGCTGGGCTAAAAGTGTATACTAATATCA  
ACACTGATGCACAAAAACAACATATGACATCTACAACAGTGATACTTAC  
ATCGCTTATCCAAACAATGAATTACAAATAGCATCTACCATCATGGATGCG  
10 ACTAATGGTAAAGTCATTGCACAATTAGGCGGGCGTCATCAGAATGAAAA  
TATTTCAATTTGGGACAAATCAATCTGTCTTAACAGACCGCGATTGGGGTTC  
TACAATGAAACCTATCTCAGCTTATGCACCTGCTATTGATAGTGGTGTCTA  
TAATTCAACAGGTCAATCATTAAACGACTCAGTTTACTACTGGCCTGGTAC  
TTCTACTCAACTATATGACTGGGATCGTCAATATATGGGTTGGATGAGTAT  
15 GCAGACCGCTATTCAACAATCACGTAACGTCCCTGCTGTCAGAGCACTTGA  
AGCCGCTGGATTAGACGAAGCAAAATCTTTCCTTGAAAAATTAGGCATAT  
ACTATCCAGAAATG

(SEQ ID NO. 92)  
MITIKKESVIKLLKYAFGIIMGFIILAIVIGLLFAYYVSRSPKLTQALKSVNSS  
20 LVDYDGNKLIADLGSEKRESVSADSIPLNLVNAITSIEDKRFFKHARGVDIYRILG  
AAWHNLVSSNTQGGSTLDQQLIKLAYFSTNKSQTLKRKSQEVWLALQMER  
KYTKEEILTFYINKVYMGNGNYGMRTTAKSYFGKDLKELSIAQLALLAGIPQA  
PTQYDPYKNPESAQTRRNTVLQQMYQDKNISKKEYDQAVATPVTDGLKELK  
QKSTYPKYMDNYLKQVISEVKQKTGKDIFTAGLKVYTNINTDAQKQLYDIYN  
25 SDTYIAYPNNELQIASTIMDATNGKVIAQLGGRHQENISFGTNQSVLTDRDW  
GSTMKPISAYAPAIDSGVYNSTGQSLNDSVYYWPGTSTQLYDWDQRQYMGWM  
SMQTAIQQSRNPVAVRALEAAGLDEAKSFLEKLGIIYPEM

30 Sequence description:

A) Length: 1386 bp - 462 aa (partial sequence)  
B) GTG start codon is preceded by an  
typical Shine-Dalgarno sequence. Possesses a  
35 potential leader peptide sequence.

40 ID-123

Clone 3-17

(SEQ ID NO: 93)  
ATGGCTAATGTATATGATTTAGCAAATGAATTAGAACGTGCTGTTTCGTGCT  
TTACCAGAATACCAAGCAGTTTTAACTGCAAAAGCAGCTATTGAAAATGA  
TGCGGATGCACAAGTGCTTTGGCAAGACTTTTTGGCTACCCAATCAAAAGT  
TCAAGAAATGATGCAATCTGGCCAAATGCCAAGTCAAGAAGAACAAGATG  
5 AAATGTCTAAACTTGGGGAAAAAATTGAATCCAATGACCTTTTAAAAGTTT  
ATTTTGACCAACAACAACGGTTGTCTGTCTATATGTCTGATATCGAAAAAA  
TTGTCTTTGCACCCATGCAGGACTTGATGTAA  
(SEQ ID NO: 94)  
10 MANVYDLANELERAVRALPEYQAVLTAKAAIENDADAQVLWQDFLATQSK  
VQEMMQSGQMPSQEEQDEMSKLGEKIESNDLLKVYFDQQQLSVYMSDIEKI  
VFAPMQDLM\*

Sequence description:

15 A] Length: 336 bp - 112 aa (full length sequence)  
B] ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. No obvious  
potential leader peptide sequence.

ID-124

25 Clone 3-26

(SEQ ID NO: 95)  
30 ATGGCAGAAATCACAGCTAAACTTGTAAGAATTGCGTGAAAAATCAGG  
TGCAGGCGTTATGGACGCTAAAAAAGCATTAGTAGAACTGATGGTGACC  
TTGATAAAGCGATTGAATTACTTCGCGAAAAAGGTATGGCTAAAGCAGCT  
AAAAAAGCAGACCGTGTTGCTGCTGAAGGTTTAAACAGGTGTTTATGTTGAT  
GGTAACGTTGCAGCAGTTATTGAAGTTAA

(SEQ ID NO: 96)  
35 MAEITAKLVKELREKSGAGVMDAKKALVETDGDLDKAIELLREKGMAKAAK  
KADRVAEGLTGVYVDGNVAIV

Sequence description:

40 A] Length: 230 bp - 76 aa (partial sequence)  
B] ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. No obvious  
potential leader peptide sequence.

ID-125

5

Clone 3-33

10 (SEQ ID NO: 97)  
ATGATAAAAAACCTGTTATTAACAGGTTTTTTATCATTTAATGACGGAAAA  
CTGGACACAAATTATTTTTCTTGTATAATTAAATATATTATTTCTTATCAGG  
AGGTTATGATGACATTAGAGAAACGATTAA

15 (SEQ ID NO: 98)  
MIKNLLLTGFLSFNDGKLDTNFYFSIIKYIISYQEVMMTLEKRF

Sequence description:

20 A] Length: 134 bp - 44 aa (partial sequence)  
B] ATG start codon is preceded by an  
typical Shine-Dalgarno sequence. Possible  
potential leader peptide sequence.

25

ID-126

Clone 3-41

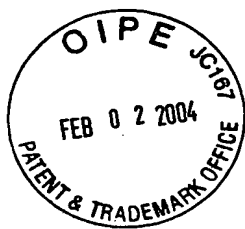
30

(SEQ ID NO: 99)  
ATGAAAAATAATAAAAAATAATGGTTTTCTGAAAAATTCCTTTATTTACATA  
TTATTGATTATTGCGGTTATTACAACCTTTCAATACTATTAA

35 (SEQ ID NO: 100)  
MKNNKNNGFLKNSFIYILLIIAVITTFQYYL

Sequence description:

40 A] Length: 94 bp - 31 aa (partial sequence)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.



ID-127

5

Clone 3-42

(SEQ ID NO: 101)  
10 ATGTTAGATATTATCTTATCCGGAATTTTCGCAAGGATTACTTTGGTCAATTA  
TGGCAATTGGCGTGTTTATCACTTTTCGTATCTTAGACATAGCCGATCTCTC  
TGCAGAAGGGGCTTCCCTATGGGGGCTGCAGTTTGCGCCTTATGTATCGT  
TAA

(SEQ ID NO: 102)  
15 MLDIILSGISQGLLWSIMAIGVFITFRILDIADLSAEGAFPMGAAVCAALCIV

Sequence description:

20 A] Length: 158 bp - 52 aa (partial sequence)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
leader peptide sequence.

25

ID-128

30 Clone 3-43

(SEQ ID NO: 103)  
ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTAATAATGAG  
TATTGATAAACTTAGATATAAAGAACCAGAGAGTGAACATGACAAGCGAC  
CTACTTTTTATTTGGTAGTACTTATACTTGTTACTGTAGCAGTTATATTGTC  
35 GTTATTAA

(SEQ ID NO: 104)  
MEMPKRNEILLNKEIKMSIDKLRYKEPESEHDKRPTFYLVVLILVTAVILSLF

40

Sequence description:

A] Length: 161 bp - 53 aa (full-length gene)  
B] ATG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential

leader peptide sequence.

ID-129

5

Clone 3-44

(SEQ ID NO: 105)  
10 GTGGTAAGTAAATTGAGTTTAAACAACGATTTTTGCATTGCTATTTTCATCA  
ATGCTAATTTACGCAACACCTCTTATCTTTACAAGTATTGGGGGAACCTTC  
TCTGAACGTGGTGGTATCGTCAACGTTGGTTTAGAAGGAATTATGGTAATT  
GGAGCTTCTCAGGCGTTGTATTAA  
(SEQ ID NO: 106)  
15 MVSKLSLTTIFALLFSSMLIYATPLIFTSIGGTFSEGGIVNVGLEGIMVIGAFSG  
VVF

20 Sequence description:

A] Length: 179 bp - 59 aa (partial sequence)  
B] GTG start codon is preceded by a  
possible Shine-Dalgarno sequence. Potential  
25 leader peptide sequence.

ID-130

30

Clone 3-46/47

(SEQ ID NO: 107)  
35 ATGAGAATTATTGCAATAACTGAAAAGGTTATAAAAGAACTGTTTCGTGAT  
AAAAGAACACTTGCTATGATGTTTTTAGCACCTATTTAATTATGTTTTTGA  
TGAATGTTATGTTTTCTGCGAATAGTAATACAAAAGTTAAGATTGGAAC  
TTAACGTTAACACGAAGGTCGTTTCAAATTTAGATAATATTAAGCATATTC  
AAGTGAGATCATTTAAATTTAACTCATCTGCTAAAAAAGCACTCAAATCAA  
40 ATAAAATTGATGCTCTTATTTTCGGAGGACAATAAATCTTATACTGTCTTCT  
ATGCGAATACAGATTCTTCAAAGACGACTTTAACAAGACAAGCTTTTAAA  
ACCGCTGTTAATACAATGAACAGTAAGGAACTGATTTTCGCAAGTTAAAATT  
TTAGCTAATAAGAATCCGAACTAGCACAATCCTTACAACTCGCTCCAAA  
TATATCAAAGAAAAATATAATTACGGAAATAAAAATACAGGCTTTTTTGC  
AAAAATGATACCAATACTAATGGGATTTATGGTCTTCTTCTTGGTTTTT



(SEQ ID NO: 108)

MRILATEKVIKELFRDKRTLAMMFLAPILIMFLMNVMFSA  
NSNTKVKIGTINV  
NTKVVS  
NL  
DNIKHQVRSFKFNSSAKKALKSNKIDALISED  
NKSYTVFYANTDS  
SKTTLTRQAFKTA  
VNTMNSKELISQVKILANKNP  
KLAQSLQTRSKYIKEK  
YNY  
GNKNTGFFAKMIPILMGFMVFFLVF

Sequence description:

- A) Length: 558 bp - 186 aa (partial sequence)  
B) ATG start codon is preceded by a possible Shine-Dalgarno sequence. Potential leader peptide sequence. C-terminus has yet to be determined.

ID-131

Clone 3-48

(SEQ ID NO: 109)

GTGATTATCGTTATGAGTAAACATCAAGAAATTTTGGAGTACCTAGAAAAT  
TTAGCTGTTGGTAAGAGGGT  
TAGTGTACGCAGTATTTC  
AAATCATTAA

(SEQ ID NO: 110)

MIIVMSKHQEILEYLENLAVGKRVS  
VRSISNHL

Sequence description:

- A) Length: 100 bp - 33 aa (partial sequence)  
B) GTG start codon is not preceded by a obvious Shine-Dalgarno sequence. No obvious leader peptide sequence.

ID-132

Clone 2-c53

(SEQ ID NO: 111)

ATGTATAGAGAAATTACCGCTGTCTGAACACGATCGCTTTGTGAGCGAATCC  
AACCAAACAAACCTACTTCAATCTCTTAATTGGCCCAAAGTAAAAGACAA  
CTGGGGTAGTCAATTACTTGGCTTTTTTGGACGGTGAAACCCAAATTGCCAG  
CGCTAGTATTCTCATCAAATCACTTCCTCTTGGCTTCTCCATGCTGTATATT  
5 CCGCGTGGACCAATCATGGATTACTCCAATCTAGATATTGTAACCTAAGGTC  
CTTAAGGACCTTAAAGCTTTTGGCAAAAAACAAAGAGCTCTCTTTATCAAG  
TGTGATCCTCTCATCTATTT

(SEQ ID NO: 112)

MYREITAVEHDFVSESNTNLLQSLNWPVKDNWGSQLLGFFDGETQIASA  
10 SILIKSLPLGFSMLYIPRGPIMDYSNLDIVTKVLKDLKAFGKKQRALFIKCDPLI  
Y

15 Sequence description:

A] Length: 326 bp - 108 aa (partial sequence)  
B] ATG start codon is preceded by an obvious  
20 Shine-Dalgarno sequence. No obvious leader  
peptide sequence.

25 ID-133

Clone 2-c59

30 (SEQ ID NO: 113)

ATGGACAAGAAAAAATCTTAGTAACGGGTATTGTGCCTAAAGAAGGTCT  
AAGAAAGCTTATGGACCGATTTGATGTTACTTATTCAGAAGATCGCCCATT  
TTCACGTGACTATGTGTTAGAGCATTTATCTGAATATGACGGATGGTTACT  
CATGGGACAAAAAGGTGATAAAGAGATGATTGATGCAGGTGAAAACCTAC  
35 AAATTATTTCTTT

(SEQ ID NO: 114)

MDKKKILVTGIVPKEGLRKLMDRFDVTYSEDRPFSDYVLEHLSEYDGWLLM  
GQKGDKE MIDAGENLQIIS

40

Sequence description:

A] Length: 215 bp - 71 aa (partial sequence)

B] ATG start codon is preceded by an obvious Shine-Dalgarno sequence. No obvious leader peptide sequence.

5

ID-134

10 Clone 2-c62

(SEQ ID NO: 115)  
ATTTTCGAAAGATGACTACCAAAATATTAGTTTTGGACAGGATCCAGAAGTT  
GTTGATTATGCTGGTCTGTTTGAAAAACGCCGTCCAGTTTTAGAAAAAGCA  
15 GTTAAAAATTTCTTGCAAGAAGAGAGAGCTACGAGAATGCTATCTGATTTC  
TTGCAAGAAGAAAAATGGGTAAGTCTGATTTTGCTGAATTTATGGCGATCAA  
AGAACATTTTGGTAATAAGGCGCTTCAAGAATGGGATGACAAGGCTATTA  
TACGCCGCGAAGAAGAAGCCTTAGCAGGATATCGTCAAAAGCTTAGTGAA  
GTGATAAAATATCATGAAGTAACGCAATATTTCTTTTACAAACAATGGTTT  
20 GAGTTAAAAGAATATGCTAATGATAAAGGGATTCAAATTATCGGTGATAT  
GCCAATCTACGTTTCTGCCGATAGTGTAGAAGTTTGGACAATGCCTGAACT  
GTTT

(SEQ ID NO: 116)  
ISKDDYQNISFGQDPEVVDYAGLFEKRRPVLEKAVKNFLQEERATRMLSDFLQ  
25 EEKWVTDFAEFMAIKEHFGNKAHQEWDDKAIIRREEEALAGYRQKLSEVIKY  
HEVTQYFFYKQWFELKEYANDKGIQIGDMPIYVSADSVEVWTMPFLF

30 A] Length: 459 bp - 153 aa (partial sequence)  
B] More sequencing is required to determine the  
N- and C-termini  
enzyme). - Streptococcus pneumoniae (63%)

35 ID-135

Identical to ID-108 described in WO 00/06736

40 Clone 2-c63

ID-136

Clone 2-c66

(SEQ ID NO: 117)

5 ATGGCAAAACAGAAAAATAACTGGCGCCGTGTTGGAGTTGGTGTCTTAC  
ACTTGCTTCAGTTGCGACTCTTGCTGCATGTGGAAGTAAATCAGCTTCCCA  
GGATTCTAATGGAGCGATTAATTGGGCTATTCCAACAGAAATCAATACACT  
AGATTTATCTAAAGTTACAGACACTTACTCAAATCTAGCTATTGGTAACTC  
TAGTAGTAATTTCTTCGCTTAGATAAAGATGGAAAGACAAGACCAGACTT  
GGCTACTAAAGTTGATGTTTCAAAAGATGGCTTAACTTATACAGCTACATT  
ACGTAAAGGCTTGAAGTGGTCAGATGGCAGTAACTTACTGCAAAGGATT  
10 TTGTTTATTCATGGCAACGTTTAGTTGATCCTAAAACAGCTTCACAATATG  
CTTACCTTGCTGTTGAAGGGCATGTGCTTAATGCCGATAAAATCAACGAAG  
GACAAGAGAAAGACTTGAATAAGCTAGGTGTTAAGGCAGAAGGCGATGA  
CAAAGTTGTTATTACTTTATCTAGTCCGTCTCCGCAATTCATCTACTACCTT  
GCATTCACTAACTTCATGCCACAAAAACAAGAAGTTGTTGAAAAATATGG  
15 AAAAGATTACGCAACTACTTCAAAAAATACAGTTTACTCAGGACCATATA  
CTGTTGAAGGTTGGAATGGTTCGAATGGTACTTTCACGCTGAAGAAAAAC  
AAAAATTATTGGGACGCTAAAAATGTAAAAACAAAAGAAGTTCGCATCCA  
GACTGTATAAAAAACCAGATACCGCCGTTCAAATGTATAAACGTGGTGAGT  
TAGATGCAGCTAATATCTCAAATACTTCTGCTATTTATCAAGCTAATAAAA  
20 ATAATAAAGATGTCACAGATGTTCTAGAAGCGACCACTGCCTATATGGAA  
TATAATACTACTGGTTCTGTGAAAGGGCTTGATAATGTTAAGATTCGTCGC  
GCCTTAACTTAGCAACTAACCGTAAAGGAGTTGTTCAAGCAGCCGTTGAT  
ACAGGCTCAAACCGGCAATTGCTTTTGCACCTACTGGTTTAGCCAAAACA  
CCAGATGGAAGTGAATTTGGCAAAATATGTTGCCCCAGGTTATGAATATAAT  
25 AAAACTGAAGCAGCAAAACTCTTTAGACTA

(SEQ ID NO: 118)

MAKQKNNWRRVGVGVLTLASVATLAACGSKSASQDSNGAINWAIPTEINTLD  
LSKVTDITYSNLAIGNSSSNFLRLDKDGKTRPDLATKVDVSKDGLTYTATLRKG  
LKWSDGSKLTAKDFVYSWQRLVDPKTASQYAYLAVEGHVLNADKINEGQEK  
30 DLNKLGVKAEGDDKVVTLSPPSPQFIYYLAFTNFMPQKQEVVEKYGKDYAT  
TSKNTVYSGPYTVEGWNGSNGTFTLKKKNKNYWDANKNVKTKEVRIQTVKKPD  
TAVQMYKRGELDAANISNTSAIYQANKNNKDVTDVLEATTAYMEYNTTGSV  
KGLDNVKIRRALNLATNRKGVVQAAVDTGSKPAIAFAPTGLAKTPDGTDLAK  
YVAPGYEYNKTEAAKLFRLL  
35

Sequence description:

40 A) Length: 1143 bp - 381 aa (partial sequence)  
B) Shine-Dalgarno sequence precedes ATG codon.  
Possesses a potential leader peptide sequence.

ID-137

Clone 2-c67

5

(SEQ ID NO: 111)

TTGAGAGTTTATGAAAATAAAGAAGAGTTGAAAAAAGAAATAAGTAAAAC  
ATTTGAGAAATACATTATGGAATTTAATAA

10 TATTCCAGAGAATCTAAAAGATAAAAGAATTGATGAAGTTGATAGAACTC  
CAGCAGAAAACCTTTCTTATCAGGTTGGCT

GGACCAACTTGGTTCTTAAATGGGAAGAAGATGAAAGAAAGGGACTTCAA  
GTAAAAACACCATCGGATAAATT

(SEQ ID NO: 120)

15 MRVYENKEELKKEISKTFEKYIMEFNNIPENLKDKRIDEVDRTPAENLSYQVG  
WTNLVLKWEEDERKGLQVKTPSDKF

Sequence description

20

A] Length: 234 bp - 78 aa (partial sequence)

B] TTG start codon is preceded by a  
potential Shine-Dalgarno sequence. No obvious  
leader peptide sequence.

25

ID-138

30

Clone 2-c70

(SEQ ID NO: 121)

ATGTCAAAGTTTGATAGTCAGAAAATAATTACTCCGATTATGAAGTTTGTC  
AATATGCGAGGGATTATTGCACTCAAAGATGGCATGCTAGCAATTTTACCA

35 CTAACAGTTGTTGGGAGTCTCTTTTAAATATTAGGGCAGCTTCCATT

(SEQ ID NO: 122)

MSKFDSQKIITPIMK FVNMRGIIALKDGM LAILPLTVVGS LFLILGQLPF

40

Sequence description

A] Length: 150 bp - 50 aa (partial sequence)

B] ATG start codon is preceded by a potential  
Shine-Dalgarno sequence. Possesses a potential

leader peptide sequence.

ID-139

5

Clone 2-c71

(SEQ ID NO: 123)  
10 GAGACCACTTCATCAGTTAAACCAGCAGGAATTGACCGTATCAATCATACC  
TCAACACCCCCGAAGAAAACCTACCCCCAACATTGCAACGACGCATAGCTT  
CAAAGATCGTTGTGATACTTTAGAAAGAATTCACAATGAAGACATTGATGT  
TTGTTCTGGATTCAATTTGTGGTATGGGAGAGAGCGATGAGGGGCTCATCAC  
ATTAGCTTTCAGACTAAAAGAAGTGAACCCCTATTCTATCCCTGTCAATTTT  
15 TTAATTGCTTAAATAATTATGGCCATGTTGCGTTTTGTTTTTCCTTTCAAGG  
AATTAAGATTAAGTGCTGGACGGGAGGTCCATTTTGAGAATTTTGAATCAT  
TAGTCACCTTACTTGTGACTCAACTTTTTTGGGAAATTACCTAACAGAGG  
GGGGTCGCAATCAACATAACCGATATTGAATTCTTGGAAAAATTACAATA  
20 AATCATACTAAAAAGGAATTAATTT  
(SEQ ID NO: 124)  
ETTSSVKPAGIDRINHTSTPPKKTTPNIATTHSFKDRCDTLERIHNEIDVCSGFI  
CGMGESDEGLITLAFRLKELNPYSIPVNFLLA VEGTPLGKYNLYLTPIKCLKIMA  
MLRFVFPFKELRLSAGREVFHFENFESLVTLVLDSTFLGNYLTEGGRNQHTDIEF  
25 LEKLQLNHTKKELI

Sequence description:

30

A) Length: 535 bp - 178 aa (partial sequence)  
B) N- and C-termini require verification

35

ID-140

Clone 2-c73

40

(SEQ ID NO: 125)  
ATGCCGGTTTGGACTGCACAGTCTATTCCAAAGGCATTTTTAGAAAAGCAT  
AATACTAAGGAAGGCACCTGGGCAAACTAACCATTCTAAGTGGTTCTTTA  
GTATTTTACCAGTTATCTCCTGATGGAGAGGAAATCTCGCGGCATATTTTT

GATGCTAGTAGTGATATTCCTTTTGTGATCCACAAGTCTGGCATAAAGTT  
TCGCCGAATAGTCCAGACTTAAGTTGCTATCTAACTTTTTACTGCCAAAAA  
GAAGATTACTTCCATAAAAAATATGGTCTCACGCGCACACATTCTGAGGTT  
ATCGCCAGTGCACCTCTCTTATCTGAGAAGAGTAATATATTAGACCTTGGG  
5 TGTGGTCAAGGGCGAAACTCACTTTATTTATCGCTGCTGGGACATCAAGTG  
ACTTCTGTTCGATTCAAACGGACAGAGCCTTGTAGCTTTAGAAAATATGGCA  
TTAGAAGAAGAGCTTCCTTACAATATAAAAAAGGTATGATATTAATACTACT  
GCTATTGAAGGGCACTATGATTTTATTTTATCAACTGTGGTATTTATGTTTT  
T  
10 (SEQ ID NO: 126)  
MPVWTAQSIPKAFLEKHNTKEGTWAKLTILSGSLVFYQLSPDGEEISRHIFDAS  
SDIPFVDPQVWHKVSPNSPDLSCYLTFCQKEDYFHKKYGLTRTHSEVIASAP  
LLSEKSNILDLCGQGRNSLYLSLLGHQVTSVDSNGQSLVALENMALEEELPY  
15 NIKRYDINTTAIEGHYDFILSTVVFMF

Sequence description:

20 A] Length: 563 bp - 187 aa (partial sequence)  
B] N- and C-termini require verification

25 ID-141

Clone 2c76

30 (SEQ ID NO: 127)  
ATGACAAAGCAAATAATTGCCATTTGGGCTGAAGATGAAGACCATTTGAT  
TGGAGTTAATGGCGGTTTACCATGGAGGCTTCCTAAAGAGTTACATCACTT  
CAAAGAAACGACCATGGGGCAGGCTTTGCTTATGGGACGAAAGACCTTTG  
ATGGAATGAACCGTCGTGTTTTACCTGGTAGAGAGACAATCATCTTAACAA  
35 AAGATGAACAATTCCAAGCAGATGGAGTGACAGTCCTAAATAGTGTTGAA  
CAAGTTATAAAATGGTTTCAGGAACATAATAAGACCTTATTTATTGTAGGT  
GGTGCAAGTATTTATAAAGCATTTCTGCCTTATTGTGAAGCAATCATAAAA  
ACTAAAGTTCATGGAAAATTCAAAGGTGATACCTATTTTCCTGATGTTAAT  
CTATCTGAGTTT  
40 (SEQ ID NO: 128)  
MTKQIIAIWAEDEDHLIGVNGGLPWRLPKELHHFKETTMGQALLMGRKTFDG  
MNRRVLPGRETIILTKDEQFQADGVTVLNSVEQVIKWFQEHNKTLFIVGGASI  
YKAFLPYCEAIKTKVHGKFKGDTYFPDVNLSEF

Sequence description:

- 5                   A] Length: 417 bp - 139 aa (partial sequence)  
                  B] ATG start codon is preceded by a Shine-Dalgarno sequence. No leader peptide sequence

10       ID-142

Clone 2-c78

15       (SEQ ID NO: 129)  
          TTGTGGCCAAACTGTGCCCCGCTTATTAATAGCACTTTGTTTCACCATTGAA  
          GATATCTTAACATCAGGTGCTCATAGCAACCCTATTTTAATGGGGGTTATA  
          CTTGGCGGGACAATTGTAGTAGTGGCGACAGCACCACCTTTCTTCTATGGCA  
          TTGACAGCTATGCTAGGATTAACCGGAATGCCTATGGCTATAGGAGCCTTG  
20       TCTGTCTTTGGTTCGTCATTTATGAATGGTGTACTTTTCCATAAATTTAAAC  
          TTGGAAGTCGTAAAGATAATATAGCTTTTGCTGTTGAGCCTCTAACTCAAG  
          CTGACGTGACTTCAGCTAACCCTATTCCAATCTATGTCACTAATTTTGTGG  
          TGGTGCAGCTTGTGGTATTTTAATTGCCTTGATGAAATTAGTTAATGATACT  
          CCTGGAACAGCGACACCAATTGCAGGATTTGCTGTCATGTTTGCCTATAAC  
25       CCAATGATAAAAGTACTAATAACCGCTCTAGGTTGTATTATCCTATCTTTA  
          CTAGCAGGCTATTTTGGAGGCATTGTTTTT  
          (SEQ ID NO: 130)  
          MWPNCAPLINSTLFTIEDILTSGAHSNPILMGVILGGTIVVVATAPLSSMALTA  
          MLGLTGMPMAIGALS VFGSSFMNGVLFHKLKLGSRKDNIAFAVEPLTQADV  
30       SANPIPIYVTN FVGGAACGILIALMKLVNDTPGTATPIAGFAVMFAYNPMIKVL  
          ITALGCIILSLLAGYFGGIVF

Sequence description:

- 35                   A] Length: 540 bp - 180 aa (partial sequence)  
                  B] N- and C-termini have yet to be elucidated

40

ID-143



Clone 2-c80

(SEQ ID NO: 131)  
5 ATGTTTTTAAGTATAATGGCAGGTGTCATAGCATTGTCTGACAGTTATT  
GCCATTCCACGCTTCATTAAGTTTTACCAATTGAAGAAAATTGGCGGGCAA  
CAAATGCATGAAGATGTCAAACAACATCTAGCCAAAGCAGGTACGCCGAC  
AATGGGAGGAACGGTATTTT  
(SEQ ID NO: 132)  
10 MFLSIMAGVIAFVLTVIAIPRFIKFYQLKKIGGQQM HEDVKQHLAKAGTPTMG  
GTVF

Sequence description:

15 A] Length: 172 bp - 57 aa (partial sequence)  
B] Shine Dalgarno sequence precedes 'ATG' start  
codon. Possesses a potential leader peptide  
sequence.

20

ID-144

25

Clone 3-83

(SEQ ID NO: 133)  
30 ATGAAACCATATTTATCTTTTATTGGTAGAACGTTATTATACTTCGGTATTT  
TATTGTTACTAATTACTTTTTTGCATACCTTGGTCGCGGACAAGGCAGTTT  
TATTTATAA  
(SEQ ID NO: 134)  
MKPYLSFIGRTLLYFGILLLLIYFFAYLGRGQGSFIY

35

Sequence description:

40 A] Length: 113 bp - 37 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.  
This orf is not in frame with nuc

ID-145

5

Clone 3-86

(SEQ ID NO: 135)  
10 ATGTCATATTTTAGAAATTACTGGTATCGTTTTGGAGCAATTTTATTTATTA  
TTTTAGCAGTAATATTGCTTGTTTTAGACCTGACTGGTCAATGCTTCACTA  
TCTATTGTATTTTACTTTATGGCACTTCTAGCGCATCAATTTGAAGAATAT  
CAGTTTCCCGGTGGGGCATCACCTATCATTAAGTATGTTGTTTATGATGAA  
GAAGAGCTGATGGATTGTTTTCCAGGCAATACTCAGTCTATTATGTTGGTT  
15 AATACTATTGCTTGGTTGCTTTACATTGCTAGTATTGCTTTTCCTCAAGCTT  
ATTGGCTTGGATTAGGAGTCATGTTCTTTAGTCTAACGCAGCTCTTGGGTC  
ATGGTTTTTCAGATGAATATTAAGTCTTAACTTGGTATAATCCTGGTCTAG  
CAACGACAGTATTTCTCCTAGTACCAATAGCTTGCGCATACATCTATCAAG  
CTAGTGCAGAAGGAATGCTCACTTGGGGAGATTGGCTAGGTGGTTTTATCA  
TGTTGATTGTCTGTGTACTAAGTACATTATTGCACCTGTACAGCTATTGAA  
20 GGATAAGGAGACCAATTATATTATTAGTCCTTGGCAAATGGACCGTTTTCA  
TAAGGTCGTTAATTTTGTAAGGATAAAAAAATAA

(SEQ ID NO: 136)  
MSYFRNYWYRFGAILFIILAVILLVFRPDWSMLHYLLYFYFMALLAHQFEEYQ  
25 FPGGASPIINYVVYDEEELMDCFPGNTQSIMLVNTIAWLLYIASIAFPQAYWLG  
LGVMFFSLTQLLGHGFQMNIKLKTWYNPGLATTVFLVPIACAYIYQASAEG  
MLTWGDWLGGFIMLIVCVLTSIIAPVQLLKDKETNYIISPWQMDRFHKVVNFV  
RIKK\*

30 Sequence description:

35 A] Length: 651 bp - 219 aa (full length gene)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.

40 ID-146

Clone 3-c88

(SEQ ID NO: 137)  
ATGCCACTTACAGCACTTGAAATTAAAGATAAAACATTTTCATCAAAATTT  
CGCGGTTATAGCGAAGAAGAAGTT

5 (SEQ ID NO: 138)  
MPLTALEIKDKTFSSKFRGYSEEEV

Sequence description:

10 A] Length: 75 bp - 25 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. No leader  
peptide

15 ID-147

20 Clone 3-90

(SEQ ID NO: 139)  
ATGTCACTTTTTCAAGAAAAAATTGCTTACAATTGCGCTAAAAAGGAAGCG  
25 CTTTATAAAGAGAGTTTAGGACGCTACGCCTTGAGATCAATGCTAGCAGG  
GGCTTATTTGACAATGAGTACTGCTGCCGGTATCGTCGCAGCTGATACTAT  
TGGTAAAATTTCTCCTGCTCTATCAGGTTTTGTATTTGCTTTTCATCTTTAGTT  
TTGGACTTATTTATGTTTTAATATTTAATGGTGAATTGGCGACATCTAATAT  
GCTTTATCTCACTGCAGGAGCCTATAATAAAAATATCTCTTGGAAAAAAGC  
CATAACAATTTTAATTTATTGTACTTTTTTCAACCTCGTTGGTGCTTGTATA  
30 TTAGCTTGGTTGTTTAA

(SEQ ID NO: 140)  
MSLFQEKIAYNCAKKEALYKESLGRYALRSMLAGAYLTMSTAAGIVAADTIG  
KISPALSGFVFVAFIFSFLIYVLIENGELATSNMLYLTAGAYNKNISWKKAITILI  
YCTFFNLVGACILAWLF

35

Sequence description

40 A] Length: 406 bp - 125 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possible  
leader peptide

ID-148

5

Clone 3-92

(SEQ ID NO: 141)  
AAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAACCAGCTTC  
10 AACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCAACCTC  
ATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAA  
TTCAGTACATAACCGTGC GGGAGATCCAGGTGATCATGGTAAAGGTTTAGC  
AGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGTTGCACA  
15 GTACTCTACACAAAATATGGCAGCAAATAACATTTTCATATGTTATCTGGCA  
ACAAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCTAATACTTG  
GAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATGACCACGT  
TCACGTATCATTTAA  
(SEQ ID NO: 142)  
KLQATEVKSV PVAQPASTTNAVA AHPENAGLQPHVAAYKEKVASTYGVNEF  
20 STYRAGDPGDH GKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQ  
KFYSNTNSIYGPANTWNAMPDRGGVTANHYDHSVHVSF

Sequence description

25

A] Length: 419 bp - 139 aa (partial sequence)  
B] N- and C-termini have yet to be determined

30

ID-149

35

Clone 3-94

(SEQ ID NO: 143)  
ATGATTCCAGTAGTTATTGAACAAACAAGTCGTGGTGAACGTTCTTATGAT  
ATTTACTCACGTCTTTTAAAAGATCGTATTATTATGTTGACAGGCCAAGTT  
40 GAGGATAATATGGCCAATAGTATCATTGCACAGTTATTGTTTCTCGATGCA  
CAAGATAATACAAAGGATATTTACCTTTATGTCAATACACCAGGTGGTTCA  
GTATCGGCTGGACTTGCTATTGTGGACACCATGAACTTCATTAAATCGGAC  
GTACAGACGATTGTTATGGGGATGGCTGCTTCGATGGGAACCATTATTGCT  
TCAAGTGGTGCTAAAGGAAAACGTTTTATGTTACCGAATGCAGAATATATG

ATCCACCAACCAATGGGCGGAACAGGCGGAGGTACACAGCAATCTGATAT  
GGCTATCGCTGCTGAGCATCTTTTAAAAACGCGTCATACTTTAGAAAAAAT  
CTTAGCTGATAATTCTGGTCAATCTATTGAAAAAGTCCATGATGATGCAGA  
GCGTGATCGTTGGATGAGTGCTCAAGAACACTTGATTATGGCTTTATTGAT  
5 GCTATTATGGAAAATAATAATTTACAATAATAGATTTAAAAGAGTTGAGTT  
TACCAACTCTTTTTTTTATTTGTTGGAATTATGTTATAATCTTAGTAATTACA  
GATATGACGCAGAAAGGAAAAAATTATTGA

(SEQ ID NO: 144)  
MIPVVIEQTSRGERSYDIYSRLLKDRIIMLTGQVEDNMANSIIAQLLFLDAQDN  
10 TKDIYLYVNTPGGSVSAGLAIVDTMNFIKSDVQTI VMGMAASMGTHASSGAK  
GKRFMLPNAEYMIHQPMGGTGGGTQQSDMAIAAEHLLKTRHTLEKILADNSG  
QSIEKVHDDAERDRWMSAQEHLIMALLMLLWKIIIYNNRFKRVEFTNSFFICW  
NYVIILVITDMTQKGKNY\*

15  
Sequence description

20 A] Length: 693 bp - 231 aa (full length gene)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. No leader  
peptide. Significantly, it would appear to have a  
very hydrophobic C-terminus.

25  
ID-150

30  
Clone 2-c86

(SEQ ID NO: 145)  
ATGAAACCAAAAaTTATTGGTGTACTTGGTCTAGGAATATTTGGACAAACA  
CTCGCACAAGAATAAGTAACCTTTGAACAAGATGTTATTGCTATTGACAGC  
AATCCTGAAAATGTACAAGCTGTCGCCGAAGT  
35 TGTTACAAAAGCAGCTATCGGAGACATTACTGATTTAGCTTTCCTAAAACA  
CATCGGGATCAGTGACTGTGATACTGTTATTATTGCTACAGGAAACAGTTT  
AGAGAGCTCAGTATTGGCCGTAATGCACTGTAAAAAGTTAGGCGTCCCAC  
AAGTTATTGCTAAAGCTCGAAACCTTGTATACGAAGAAGTACTTTATGAAA  
TTGGTGCTGATTTGGTTATCTCTCCGGAGCGAGAATCTGGGGCAAATGTTG  
40 CTGCAAACCTCATGAGAAATAAAATTACAGATGTCTTCCAGATTGAATCTG  
ATATTTCTGTCAATTGAATTT

(SEQ ID NO: 146)  
MKPKIIGVLGLGIFGQTLAQELSNFEQDVIAIDSNPEN VQAVAEVVTKAAIGDI  
TDLAFLKHIGISDCDTVIIATGNSLE

SSVLAVMHCKKLGVPQVIAKARNLVYEEVLYEIGADLVISPERESGQNVAAN  
LMRNKITDVFQIESDISVIEF

5 Sequence description:

10 A] Length: 459 bp - 153 aa (partial sequence)  
B] Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. Possesses a  
potential leader peptide sequence.  
This orf is not in frame with nuc

15 ID-151

20 Clone 2-c88

(SEQ ID NO: 147)  
GTGCGTTATAGTAAAGAGATTATTCAGTTAGCTATACCAGCTATGATTGAA  
AATATCTTACAAATGCTCATGGGAGTAGTTGATAATTATCTAGTGGCTCAG  
TTAGGTGTTGTAGCAGTATCAGGTGTTTCAGTTGCTAATAATATAATTACT  
25 ATTTATCAAGCTATTTTTATAGCTTTAGGGGCGAGTATAGCAAGTCTATTG  
GCCAAGTCGTTAGCAGGTAGTGAGAAGGATGATGCAATTTTCAGTATGTTCT  
CAAGCCATTTTTCTAACATCACTGATAGGGGCAGTATTAGGAATTATCTCG  
ATTGTTTTTTGGACAAACTTTCTTT

(SEQ ID NO: 148)  
30 MRYSKEIIQLAIPAMIENILQMLMGVVDNYLVAQLGVVAVSGVSVANNIITIY  
QAIFIALGASIASLLAKSLAGSEKDDAISVCSQAIFLTSLIGAVLGIISIVFGQTF

35 Sequence description

40 A] Length: 330 bp - 110 aa (partial sequence)  
B] Putative GTG start codon is preceded by a  
typical Shine-Dalgarno sequence. May have a  
leader peptide

ID-152

Clone 2-c92

5

(SEQ ID NO: 149)

TTGATTAAACAAGTATTCGTGCTTTTTGAAGAGGATTCTCCATAATAATACT  
CCTTTAATAGTTATCGTGAGAAGTATTTTAAAGAAAAACCGCCAAGGTAG  
AGCGACATTTCTGCCTTTAACTACAATAAAACCAAGAGAATTAGCACAAAC  
ATTATCTCTCAAAATTACAAAGTTCTCAAGGGTTTTTAGGAATAGCTAGTG  
AATTGGTAACCTATGATCAACGCTTGTCAAACATTTTT

10

(SEQ ID NO: 150)

MINKYSCFLKRILHNNTPLIVIVRSILKKNRQGRATFLPLTTIKPRELAQHYLSK  
LQSSQGFLGIASELVTYDQRLSNIF

15

Sequence description

A] Length: 240 bp - 80 aa (partial sequence)

B] No obvious Shine Dalgarno sequence precedes the Putative TTG start  
codon

20

ID-153

25

Clone 2-c94

30

(SEQ ID NO: 151)

TTGTTGACTCACAAAAATATATTATTAACCATTATATTTGGATTATTTATGA  
TTATATTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATA  
ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTTGATAAT  
ACTTTTGTTTCTATGGGATTTGAAAGTCGTTCTGGTGACTATACCGGCTTTG  
ATATTGATTTAGCTAATGCTGTTTTTAAAGAATACGGTATTTTCAGTGAAAT  
GGCAGCCTATTAACCTGGGATATGAAAGAACTGAACTTAATAATGGTAAT  
ATAGACCTTATTTGGAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAA  
AGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAA  
AACTTCATCACATATTAATAGTATTAAGGATATGAAGGGGAAAAAACTAG  
GAGCCCAGTCGGGTTTATCTGGTTTTGATGCTTTTAACGCTAAACCTGATA  
TTTTAAAAAAGTTTGTAAGGAAAAGAAGCAGTTCAATACGATACTTTC  
ACTCAGGCTTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTTGATT  
GATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGAA

40

(SEQ ID NO: 153)

MLTHKNILLTIIFGLFMILSACGMSNKEMAGIDNWEHYQKEKKITIGFDNTFV  
PMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKETLNNGNIDLI  
WNGYSKTAERAKKVAFTNPYMNNHQVIVTKTSSHINSIKDMKGKKLGAQSG  
SSGFDAFNAKPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANY  
YLKQEG

Sequence description

A] Length: 649 bp - 216 aa (partial sequence)  
B] TTG start codon is preceded by a possible  
typical Shine-Dalgarno sequence. Has a  
leader peptide

ID-154

Clone 2-c100

(SEQ ID NO: 153)

ATGAAAATTTGGAAAAAATAACCTTAATGTTTTCTGCAATTATTTTAACA  
ACAGTAATTGCATTGGGAGTCTATGTTGCCTCAGCTTATAATTTTTCGACTA  
ATGAATTGTCTAAGACTTTT

(SEQ ID NO: 154)

MKIWKKITLMFSAILTTVIALGVYVASAYNFSTNELSKTF

Sequence description

A] Length: 123 bp - 41 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Has a  
typical leader peptide

ID-155

Clone 2-c1



(SEQ ID NO: 155)  
ATGAAAAACAAAGACTATTACTGCTTTTTGGAGGCTTATTAATAATGATA  
ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAA  
5 GGAATACCAGGCAGAACAGAATTTTAAGTCATACTTTAAATATATATCAG  
ATAAAAATAACTATTTAGATAATATAAAAGTTTATTACTTTTCTATAAGTA  
TTTCTAAAGATGTACAAGATAAAGTCAGTGAAACAACAACCTTGTTTCATATA  
GACTAGAAAAGCAAAAAGAATCAAGAGTTCATTGGTAATTTTGAACATGAA  
GTTAGTGAATCTAGTCAATATTCAACCGAAGTTAAAAATCAAATACAGTAT  
10 CCAATCCAGTATAAAGATAATTCAATTCGTTTTACTGAAAAAACACCGTCA  
GAACGTTATGATGAGTTTGTTTTAGTTCATTTGATTCTTCATTATTAATAA  
AATATAAAATATATGATTACTTACTAAAACATCCCGAAACTGAATTAATA  
GGTGTTTCCTATAAGATTCCTATAAATTCTGAAATTGTAGCCCCTTTTATAA  
ATCAATTAAATATAAAAAATCCTAAAAAATCATCTATTTTCGGTTACAAAAA  
15 CGGAAAGTAAAGAATATTATTATACAATCAGTATTGATACTGATTCTGAGA  
TATATTCTATATTCTGAAGGTATTCAT

(SEQ ID NO: 156)  
MKKQRLLLLFGGLLMIMMTACKDSKIPENRTKKEYQAEQNFKSYFKYISDKN  
NYLDNIKVVYFISISKDVQDKVSETTTCYSRLEKQKNQEFIGNFEHEVSESSQ  
20 YSTEVKNQIQYPIQYKDNSIRFTEKTPSERYDEFVSSFDSSLLKKYKIYDYLLK  
HPETELKGVSYKIPINSEIVAPFINQLNIKNPKKSSISVTKTESKEYYYTISIDTDS  
EIYSIFEGIH

25 Sequence description

30 A] Length: 687 bp - 229 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Has a  
typical leader peptide. C-terminus has yet to be  
verified

35 ID-156

Clone 2-c5

40 (SEQ ID NO: 157)  
ATGACATTGACACCATTGATCAATTAGCGGTTAATACAGTCCGCACGCTT  
TCTATTGATGCTATCCAAGCAGCAAATTCTGGGCACCCAGGTCTTCCTATG  
GGAGCTGCGCCTATGGCTTATGTGCTTTGGAATAAATTCTTAAATGTAAAC  
CCAAAAACAAGTCGCAATTGGACAAACCGTGACCGTTTTGTACTTTCAGCT

GGGCATGGTTCAGCTCTTCTTTATAGCCTACTTCATTTAGCTGGCTATGATT  
TATCAATTGATGATTT

(SEQ ID NO: 158)  
MTFDTIDQLAVNTVRTLSIDAIQAANS GHPLPMGAAPMAYVLWNKFLNVNP  
KTSRNWTNRDRFVLSAGHGSALLYSLHLAGYDLSIDD

Sequence description

10

A] Length: 272 bp - 90 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. No obvious  
leader peptide

15

ID-157

20

Clone 2-c8

(SEQ ID NO: 159)  
ATGAGAACACTATTTAGAAATGATATTTGCTATTCCAAAGTTTATCTTTAGA  
TTGATTTGGAATATCATTGTTGGGGAATATTCAAGACAGTTCTTGTTATTGCG  
ATTATTTTATTTGGCTTGTATTACTATGCGAATCACAGTCAATCAGAATTTG  
CTAATCAACTAGTGACATTATTCAGACAGGAAAAACATTTTT

25

(SEQ ID NO: 160)  
MRTLFRMIFAIPKFIFRLIWNIIWGIFKTVLVIAILFGLYYYANHSQSEFANQLS  
DIIQTGKTF

30

Sequence description

35

A] Length: 197 bp - 65 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

40

ID-158

Clone 2-c9

5 (SEQ ID NO: 161)  
ATGTCAAAAAAAAAATAATATTAGGAATTTTATCTCTTTTATCTGTCGTTACTT  
TGGTGGCGTGTGGTTCATCAGACAAACAGCTACAAGATAAAGTTGAGAAA  
AAAGGGAAGTTAGTTTTAGCGGTGAGTCCAGATTATGCTCCCTTTGAGTTT  
10 (SEQ ID NO: 162)  
MSKKIILGILSLLSVVTLVACGSSDKQLQDKVEKKGKLVLA VSPDYAPFEF

Sequence description

15 A] Length: 153 bp - 51 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide (not in frame with nuc)

ID-159

25 Clone 2-c10

(SEQ ID NO: 163)  
ATGAAAAATCAAAGACTATTACTGCTTTTTGGAGGCTTATTAATAATGATA  
ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAA  
30 GGAATACCAGGCAGAACAGAATTTTAAGTCATACTTT  
(SEQ ID NO: 164)  
MKNQRLLLLFGGLLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYF

35 Sequence description

40 A] Length: 139 bp - 46 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

ID-160

Clone 2-c11

5

(SEQ ID NO: 165)  
ATGATTGGAAAATTATATTATAGCTATAGAAAGTCACGCTTATTAAGAAGT  
ATTTTATGGCTTATTTTAATTGTTGGTGTATATATGTTAGGACAACGTGTTT  
TATTATCCACTGTTTCCTTTATCACATCAAGAGATAAACTAGCAGTAGATC  
10 AACATTTACTCAATAACTTTTCAGCAGTAAGTGGTGGGAGTTTTAATAAAT  
TAAATGTTTTCACACTGGGGTTGAGTCCATGGATGTCAAGTATGATTATTT  
GGAGATTCGTTTCCTTATTTTCGTGGGCAAAAAATGCAACGAAGCGAAAA  
GCAGAAGTAGCTCAATATACTTTAATGCTTACTATCTCAGTTATACAAGCA  
TATGGTGTTCAGGAAATCAATTTATAAAAAGCTCTTTATTAGGTTCTTATA  
15 GTGATATTGTTTTT

(SEQ ID NO: 166)  
MIGKLYYSYRKSRLRLRSILWLILIVGVYMLGQRVLLSTVPLSHQEIKLAVDQHL  
LNNFSAVSGGSFNKLVFTLGLSPWMSSMIIWRFVSLFSWAKNATKRKA EVA  
QYTLMLTISVIQAYGVSGNQFIKSSLLGSYSDIVF  
20

Sequence description

25 A] Length: 423 bp - 141 aa (partial sequence)  
B] ATG start codon is preceded by a potential  
typical Shine-Dalgarno sequence. Possesses a  
leader peptide

30

ID-161

35 Clone 2-c13

(SEQ ID NO: 167)  
ATGAAAGGTCTATTGGATTTTTTAGTTAATATTGCCAGAACGCCAGCTATT  
T TAGTCGCCTTGATAGCCATTATCGGTTTAGTACTGCAGAAAAAAGGTGTT  
40 CCTGATATTGTAAAAGGTGGAATAAAAAACATTTGTTGGCTTCTTAGTGGTT  
TCTGAAGGTGCAGGGATAGTCCAAAATTCCTTGAATCCATTTGGAAAAATG  
TTTGAACATGCTTTTCATTTGGTGGGGGTAGTTCCTAATAATGAAGCCATT  
GTAGCAGTAGCTCTTACGAAGTATGGCTCAGCAACTGCTTTGATTATGTTA  
GCGGGAATGATTTTTAATATTTTAATTGCTCGTTTTACAAAA

(SEQ ID NO: 168)  
MKGLLDFLVNIARTPAILVALIAIIGLVLQKKGVDPDIVKGGIKTFVGFLVVSEG  
AGIVQNSLNPFGKMFEHAFHLVGVPNNEAIVAVALTKEYGSATALIMLAGMI  
FNILARFTK

5

#### Sequence description

- 10                   A] Length: 348 bp - 116 aa (partial sequence)  
                  B] ATG start codon is preceded by a potential  
                  Shine-Dalgarno sequence. Possible leader  
                  peptide

15

ID-162

Clone 2-c21

20

(SEQ ID NO: 169)  
TTGGTTGGTAAGCCCCAATTACTATTTTTAGATGAACCTACTTCCGGAATG  
GATACTTCCACACGTCAACGATTTTGGAAGCTGGTTGCGACACTAAAAAA  
AGAAGGTGACACAATTGTCTATTCTAGTCATTATATCGAAGAGGTAGAAC  
25                   ATACAGCTGATAGGATTTTAGTACTTCATAAAGGAAAGTTATTACGCGATA  
                  CAACCCCTTTGCCATGAAGCAAGAAAAAACCGAAAAGTTATTCACCGTT  
                  CCGCTTAGTTATCAAAAATTATTACCTACCTATTTGATTACAGAGTGTGAA  
                  GCCAAGAGTGATAGTATAACGTTTGTTACTGGGGAGGCTGAAACTGTATG  
                  GAAAATACTGGCAGATAATGGTTGTCCTATTGAAGCTATTGAGATGACCA  
30                   ATAGAACTTTGTAAATCGTATTTTTGAGACTACTAAGGAGGTAAACATG  
                  AGAATCTTTA

30

(SEQ ID NO: 170)  
MVGKPQLLFLDEPTSGMDTSTRQRFWKLVLKKEGDTIVYSSHYIEEVEHTA  
DRILVLHKGKLLRDTPFAMKQEKTEKLFTVPLSYQKLLPTYLITECEAKSDSI  
35                   TFVTGEAETVWKILADNGCPIEAIEMTNRTLLNRIFETTKEVKHENL

35

#### Sequence description

40

- A] Length: 462 bp - 155 aa (partial sequence)  
B] B] Putative TTG start codon is not preceded by  
an obvious Shine-Dalgarno sequence. No obvious  
leader peptide. N- and C- termini require further



examination.

ID-163

5

Clone 2-c25

(SEQ ID NO: 171)  
10 TTGAAAAAATCCCAAGAGAAGCCGTAAGGCAGTGACAACAAGTGGTGAGA  
AGACTTTACTTGAGGATTTGGCAAAAATGAATTTCTAGACGAAGTCATTA  
ATGTTATGGTTTTATATACCTTGAATAAGACAAAATCTGCTAACTTAAATA  
AGGCCTATATCATGAAAGTTGCTAATGATTTTGCCTTTCAGAATGTTATGA  
CGGCCGAAGATGCTGTGCTTAAAATTCGTGATTTTTCAGATCAAAAAGTAA  
15 GGACTAAAACAGAAACGAAGAAGAAACAATCGAATGTTCTGAATGGAGT  
AATCCTGATTATAAAGATGAGGTTAGCCCAGAAAAAGAAATTGAATTAGA  
ACAGTTT  
(SEQ ID NO: 172)  
20 MKKSKRSRKAVTTSGEKTLLEDLAKMNFLEVINVMVLYTLNKTksANLNK  
AYIMKVANDFAFQNVMTAEDAVLKIRDFSDQKVRTKTETKKKQSNVPEWSN  
PDYKDEVSPKEIELEQF

Sequence description

25

A] Length:360 bp - 120 aa (partial sequence)  
B] N- and C- termini require verification.

30

ID-164

Clone 2-c28

35

(SEQ ID NO: 173)  
ATGACGAATCATATTACTAAACTGATAGAAAATAGCGGAAAAAAATTGAC  
AGAAATTAGCGAAGCTACAGATATAGCCTATCCTACACTTTCTGGATACAA  
TCAAGGAATCCGCAAACCTAAAAAAGATAATGCTGAAAAATTGGCAAAAT  
40 ACTTTAATGTTTCCGTCGCTTACATTATGGGACTTGATAGCAACCCACATG  
CTCCATCAAATCTT  
(SEQ ID NO: 174)  
MTNHITKLIENSGKKLTEISEATDIA YPTLSGYNQGIRKPKKDNAEKLAKYFNV  
SVAYIMGLDSNP HAPSNL

Sequence description

5

A] Length:218 bp - 72 aa (partial sequence)  
B] ATG start codon is preceded by an  
obvious Shine Dalgarno sequence. No obvious  
leader peptide.

10

ID-165

15

Clone 2-c29

(SEQ ID NO: 175)  
TTGATGAAAAGGAATAAACATTTACCGTTAACAGAACTACCTATTATATT  
20 TTATTAGCTTTGTTTGAGGAAGCGCATGGCTATGCTATTATGAAAAAAGTT  
GAAGAAATGAGTGGCGGTGATGTTAGAATAGCCGCAGGGACAATGTACGG  
TGCCATTGAAAATTTACTTAAACAAAAATGGATAAAGTCTATCTCAAGTGA  
CGATAGAAGAAGAAAAGTTTATATTATTACTGAGACAGGAAAAGAAATAG  
TAGAACTTGAAACGAATCGATTAAGAAAGTTACTTAATACTGCTAATCAGT  
25 TGGGTTTTGGAGGAGATGGTTATGATAAAGTTT  
(SEQ ID NO: 176)  
MMKR NKHLPLTETTYI LLALFEEAHGYAIMKKVEEMSGGDVRIAAGTMYG  
AIENLLKQKWIKSISSDDRRRKVYIITETGKEIVELETNRLRKLNTANQLGFG  
GDGYDKV

30

Sequence description

35

A] Length:337 bp - 112 aa (partial sequence)  
B] TTG start codon is preceded by an  
obvious Shine Dalgarno sequence. Actual start  
codon may ATG that comes immediately after the  
TTG. Potential leader peptide.

40

ID-166

Clone 2-c35

(SEQ ID NO: 177)  
5 CCCATTACTGGTGAGTTAATAGCTGAGAAATTAGGAGTACCAAGAGCAGC  
ACTAAGGTCTGATTTGCGGGTTTTAAGTATGCTAGGTATCATAGATGCAAA  
ACCTAAGGTTGGTTATTTTTATTTAGGACAGTATCATGCTTCAATAGGGAC  
AAGTCATTTTGAAAAGATGACAGTTTCAGAAATTATGGGGATCCTTCTGAC  
AGTTCATCAAAAAGATTTCAGTTTATGATGTTATTGTACATATTTTTATGGA  
10 AGATGCTGGTTGTGCTTTTATCTTGGATGATGATGATTTTCTCTGTGGAGTC  
GTGTCACGTAAAGATTTACTAAAAACCAGTATTGGCGGAGGAGATCTTTCT  
AAAATGCCAATAGGAATGGTGATGACACGTATGCCACACGTGACAACGT  
TTTAGAAAATGAAAGTCTTTTTGCGGCAGCTGATAAATTAGTGAGCAGAA  
AAGTGGATAGTCTCCCTGTCGTTTCGTCATGATAAGCAATATCCCGAAAAAT  
15 TTA  
(SEQ ID NO: 178)  
PITGELIAEKLGVPRALRSDLRVLSMLGIIDAKPKVGYFYLGQYHASIGTSHF  
EKMTVSEIMGILLTVHQKDSVYDVIVHIFMEDAGCAFILDDDDFLCGVVSRKD  
LLKTSIGGGDLSKMPIGMVMTRMPHVTTVLENESLFAAADKLVSARKVDSL  
20 VRHDKQYPEKF

Sequence description

25 A] Length:511 bp - 170 aa (partial sequence)  
B] N- and C-termini to be determined

30 ID-167

35 Clone 2-44

(SEQ ID NO: 179)  
TTGGAAGTCATCATGCAATTTATTTATAGTATTATTGGTATTTTATTGGTAT  
TAGGAATTGTGTATGCAATTTCTTTCAATCGTAAGAGTGTTTCTCTAAGTTT  
AATTGGAAAAGCTCTTATCGTTCAATTCATTATTGCGCTAATCTTAGTACGT  
40 ATCCCACTAGGCCAACAAAGTTGTTAGTGTTGTTTCAACTGGAGTTACTAAA  
GTAATCAACTGTGGTCAAGCTGGTTT  
(SEQ ID NO: 180)  
MEVIMQFIYSIIGILLVLGIVYAISFNKRSVLSLIGKALIVQFIALILVRIPLGQQ  
VVSVVSTGVTKVINCGQAG



Sequence description

5

A] Length:233 bp - 77 aa (partial sequence)  
B] TTG start codon is preceded by a  
possible Shine Dalgarno sequence. Actual start  
codon may occur further downstream. Potential  
leader peptide.

10

ID-168

Clone 2-46

15

(SEQ ID NO: 181)  
CAACCTAATAAAGCTTTAGAAAGTGATGAGATTGATATTAATGCTTTCCAG  
CATTATAATTACTTAACCAATTGGAATAAAGCAAATAAGACCAATCTTGTT  
TCCGTTGCTGAGACATACTTTACTTCCTTTAGATTATACTCTGGTACTAAGA  
ACGGTAAAGGTAAATACCAAACAGTTTCTGAAATTCCAAATAAAGCAACT  
ATTACTATCCCAAACGATGCAGTTAACGAAAGTCGCTCTCTCTACTTGTTA  
CAATCAGCAGGCTTGCTAAAATTGAAAGTATCAGGTGATACATTAGCAAC  
AATGTCAGATGTTGTTTCCAATCCTAAATCTTTAGATTT

20

25

(SEQ ID NO: 182)  
QPNKALESDEIDINAFQHYNLTNWNKANKTNLVSVAETYFTSFRLYSGTKN  
GKGKYQTVSEIPNKATITIPNDVNESRSLYLLQSAGLLKLKVSGDTLATMSD  
VVSNNPKSLD

30

Sequence description

A] Length:344 bp - 114 aa (partial sequence)  
B] N- and C- termini require verification

35

ID-169

40

Clone 2-47

(SEQ ID NO: 183)  
ATGAAATGTATAATAAATAATATAAATAAAATAAAAATGATAATTGAGAT  
TTATCATAGAAGGAAAACATTTTGAATTAAATAAAATCATATTATCTAC

TGCAGCTCTTACTGCTCTCTTTTTAGGATATAATAGCGTTACTGCGGATACA  
TATAATAACTATCAGCCACATAGATCAAATAATATGGATTTAACTGAGGA  
ATATAACTATAATAACCAGATAGAACTTCAGGAGCGTATAAAAAACCTAA  
ATATACCTTTT

5

(SEQ ID No: 184)

MKCIINNINKIKMIEIYHRRKTILKLNKIILSTAALTALFLGYNSVTADTYNNY  
QPHRSNNMDLTEEYNNYNQIELQERIKNLNIPF

10

Sequence description

A] Length:264 bp - 88 aa (partial sequence)

B] There is a Shine-Dalgarno sequence upstream  
of this sequence. Potential leader peptide  
sequence

15

20

ID-169

Clone 2-47

25

ATGAAATGTA AATAAAATAAAAAATGATAATTGAGAT  
TTATCATAGAAG TGAAATTAAATAAAATCATATTATCTAC  
TGCAGCTCTTACTG TAGGATATAATAGCGTTACTGCGGATACA  
TATAATAACTATCAGCC AGATCAAATAATATGGATTTAACTGAGGA  
ATATAACTATAATAACCAGATAGAACTTCAGGAGCGTATAAAAAACCTAA  
ATATACCTTTT

30

MKCIINNINKIKMIEIYHRRKTILKLNKIILSTAALTALFLGYNSVTADTYNNY  
QPHRSNNMDLTEEYNNYNQIELQERIKNLNIPF

35

Sequence description

40

A] Length:264 bp - 88 aa (partial sequence)

B] There is a Shine-Dalgarno sequence upstream  
of this sequence. Potential leader peptide  
sequence

ID-170

5 Clone RS-58b

(SEQ ID NO: 185)  
TTGGGTGATTATTATGGTAAGAAATATTTTGGTGAGGCAGCTAAAAAAGA  
CGTCGAACATATGGCTAAGAAAATCATTAATGTCTATAAAACACGGTTAA  
10 AAAACAACACTTGGTTATC  
AGAAAATACAAAAGCAATGGCCATTAAGAACTTGATAACATGAGATTAA  
TGATTGGCTATCCAGAAGATTATCCTGATCTTTATCGTCAGTACCAATTTG  
ATAGTAAAGCAAGCTTCTTTGAAAACAATGATAACTACAGAAAATTATCG  
AACAAGAAAACATTTGAAGAATTTAACCAGTCTAATCAACGTGAACATTG  
15 GCAATGAGTGCCAATGCTGTAAATGCTTATAATGATCCTAATACCAATTC  
CATAGTCTTTCCAGCAGCGATTTTTCAATCACCAGTGTACGATAAACTAA  
AACAGTTAGTCAAAATTATGGAGCTATCGGAGCAATTATTGGTCATGAAAT  
TTCACACTCATTTGATATTAATGGTATGAAATATGACGAGAAAGGGAATCT  
TCACGATTGGTGGACTAAAGAAGATTTAAATCATTATAAGAAATCAACAC  
20 AAGCTATGATTGACCAATGGGATGGCCTTAAAGCAGATGGCGGTAAAGTT  
GATGGTAAATTAAGTTTAGCAGAAAATATTGCAGATAATGGTGGTGTATG  
GCATCTCTAGAAGCTCTTAAGACTGAAAAAATCCAACTATAAAGAATTTT  
TTGAATCATGGGCAAGTATTTGGCGTCAAAAAGCAACCAAAGAACAAGT  
AAGTCCTCAATTCAGTCAGATGTTTCATGCACCATATGAATTGA  
25 GAGCTAACATCCCAGTACGTAATTTCCAAGAATTTTATGATGCCTTTGGTG  
TTAAAAAAGGCGATTCAATGTATCTAAAACAGAAAAACGTTTGACACTTT  
GGTAA

(SEQ ID NO: 186)  
30 MGDYYGKKYFGAAKKDVEHMAKKIINVYKTRLKNNTWLSSENTKAMAIKK  
LDNMRLMIGYPDYPDLRQYQFDSKASFFENNDNYRKLSNKKTFEEFNQSNQ  
REHWQMSANAVNAYNDPNTNSIVFPAAIFQSPLYDKTKTVSQNYGAIGAIIGH  
EISHSFDINGMKYDEKGNLHDWWTKEDLNHYKKSTQAMIDQWDGLKADGG  
KVDGKLTLAENIADNGGVMASLEALKTEKIQTIKNFLNHGQVFGVKKQPKNK  
35 VSPQFSQMFMHHMN\*

Sequence description:

40 A] Length: 819 bp - 272 aa (full length gene)  
(107 bp of additional DNA sequence (> onwards) is  
also included. While not in-frame with the  
described orf, it also shares strong homology  
with the neutral peptidases.

→  
B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-89 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-89 gene sequence. ID-89 and ID-170 together show homology over their combined entire length with the neutral endopeptidases from *Lactococcus* and *Lactobacillus*. Possesses TTG (possible ATG start codon located 13 bp further downstream) start codon with no obvious signal peptide. Shine Dalgarno sequence not immediately obvious. Possibly located further downstream

10 ID-171

Clone 2-18/22b (Mod2)

15 (SEQ ID NO: 187)  
ATGACCATGATTACGCCAAGCTTCATTAAGGTATCTCTAGATGAAACAAAT  
CGTATGATGCGTATGATATCAGATTTATTAAGTTTATCGCGCATTGATAAT  
GAAGTAACGCATTTAGATGTTGAAATGACGAATTTTACAGCTTTCATGACC  
TCAATTTTGAATCGATTTGATCAGATTAGAAATCAAAAAACAGTCACAGG  
20 AAAAGTTTATGAAATTGTCAGAGATTATCCTCTTAAGTCAATTTGGGTGGA  
AATTGATACAGATAAGATGACTCAAGTGATTGATAACATTTTAAATAATGC  
AGTCAAGTATTCACCAGATGGTGGTAAGATTACAGTTAATCTACGCACAAC  
TAAACGCAGATGATTTTATCAATATCAGACCAAGGCTTAGGTATTCCCAA  
AAAAGATTTACCTCTCATTTTTGATCGTTTTTATCGTGTTGATAAGGCGAGA  
25 AGTCGTCAACAGGGTGGGACTGGACTTGGTTTGTCAATTGCAAAAGAAAT  
TGTTAAGCAGCATAAGGGATTTATTTGGGCTAAGAGTGAGTATGGTAAAG  
GGTCTACTTTTACAATCGTCTTGCTTATGATAAAGATGCTGTAACCTTATGA  
AGAATGGGAGGACGTTGAAGATTAA

30 (SEQ ID NO: 188)  
MTMITPSFIKVSLEDETNRMMRMISDLLSLSRIDNEVTHLDVEMTNFTAFMTSIL  
NRFDQIRNQKTVTGKVYEIVRDYPLKSIWVEIDTDKMTQVIDNILNNAVKYSP  
DGGKITVNLRTTKTQMILSISDQGLGIPKKDLPLIFDRFYRVDKARSRQQGGTG  
35 LGLSIAKEIVKQHKGFIWAKSEYGKGSTFTIVLPYDKDAVTYEEWEDVED\*

Sequence description:

40 A] Length: 613 bp - 212 aa (full-length gene possibly)  
B] Possible Shine Dalgarno sequence present  
upstream of a ATG start codon. May not have yet  
determined the N- portion of this gene. No  
obvious signal peptide.

ID-172

5

Clone 2-54balternate (107b)

(SEQ ID NO: 189)  
10 TTGAAAAAAATTATTACTTCTATTCTATTACTTAGTTGCATTTTTTTTATGC  
CAACCATCTCTGCTGAATCTTTTAATGCTTCCGCTAAACATGCCTTAGCAGT  
TGATTAGATTCAGGAAAAATCTTGTATGAAAAAGATGCTAACAAACCCG  
CTGCTATTGCTTCCTTGACTAAAATAATGACCGTTTATATGGTCTATAAAG  
AAATTGATAACGGTAACCTCAAGTGGAATACCAAAGTAAATATATCTGAC  
15 TACCTTATCAACTAACACGCGAATCTGATGCTAGTAATGTTCCCTTAGAA  
AAAAGGCGCTATACTGTAAACAACCTCGTGGACGCTGCCATGATTTCTAGT  
GCTAACAGTGCAGCCATTGCTTTAGCTGAACATATTTTCAGGAACTGAAAGT  
AAATTTGTTGATAAAATGACTGCTCAATTGGAAAAGTGGGGAATTCATGAT  
AGCCACCTAGTCAATGCTTCTGGCTTAAATAATAGTATGTTAGGCAATCAC  
ATTTATCCAAAATCGTCACAAAACGACGAAAATAAAATGAGTGCACGTGA  
20 TATTGCTATTGCTGCCTACCATTGTTGCTCAACGAATATCCTTCCATTCTTAAG  
ATTACTAGTAAGTCCGTTGCTAAATTTGATAAAGATATTATGCATTCTTAT  
AACTACATGCTACCAGATATGCCTGTCTTTAGACCAGGTATTACAGGTTTG  
AAAAGTGGGACAACGGAATTAGCTGGCCAATCTTTTATTGCTACATCTACT  
GAAAGTGGAAATGAGACTACTCACTGTTATTATGCATGCTGATAAGGCCGAT  
25 AAAGACAAATATGCTCGCTTTACAGCAACTAACTCTCTCTTGAACATATC  
ACAAACACCTACGAACCTAACCTTGTATTAGCTAAAGGAGCTGCATATAA  
AGGTAAAGAAGCAAGTGTGAGAGACGGAAAAGAACAATCGGTCATCGCT  
GTTGCTAAAAACGATTTGAAAGTAGTACAGAAGAAAAATATCACTAAACA  
AAATCAGTTAAAAATTAACTTTAAAAAAGAGCTTACTGCTCCTATTACAAA  
30 AAAAGAGAACCTAGGGAAAGCTTATTACGTTGACCTTAATAAGGTTGGAA  
AAGGCTATCTCATAAAGGAACCTAGCGTTCATTTAGTGGCAAAGATAGT  
ATTGAGCGCAGTTTCTTCCTCAAAGTGTGGTGAATCATTTTGTGCGCTAC  
GTTAACGAAAAACTTTAA

35

(SEQ ID NO: 190)  
MKKIITSILLLSKIFFMPTISAESFNASAKHALAVDLDSGKILYEKDANKPAAIA  
SLTKIMTVYVMVYKEIDNGNLKWNTKVNISDYPYQLTRESNASNVPLEKRRT  
VKQLVDAAMISSANSAAIALAEHISGTESKFVDKMTAQLEKWGIHDSHLVNA  
SGLNNSMLGNHIYPKSSQNDENKMSARDIAIAAYHLVNEYPKILKITSKSVAKF  
40 DKDIMHSYNYMLPDMFVFRPGITGLKTGTTELQSFQIATSTESGMRLTLVIM  
HADKADKDKYARFTATNSLLNYITNTYEPNLVLAKGAAYKKGKEASVRDGKE  
QSVIAVAKNDLKVVQKKNITKQNQLKINFKKELTAPITKKENLGKAYYVDLN  
KVGKGYLIKEPSVHLVAKDSIERSFFLKVWWNHFVRYVNEKL\*

Sequence description:

- 5           A] Length: 1236 bp - 412 aa (full-length gene sequence possibly)  
            B] A possible Shine-Dalgarno sequence precedes the putative 'TTG' start  
            codon. (needs further cloning and sequencing to verify N-terminus)

ID-173

10

Clone 3-60b

(SEQ ID NO: 191)  
15   ATGACGCTTCGAGAATTAACAATAGAAGAATTTAAAGAACATTCAGGAAA  
TTATGATTCACAATCATTTTTACAAACACCTGAGATGGCTAAACTTTTAGA  
AAAACGCGGCTATGATGTTAGGTATTTGGGATATCAAGTAGAAAATAAAC  
TAGAGATAATCAGTTTATCTTATATTATGCCAGTCACTGGTGGTTTTCAAAT  
GAAAATTGATTCAGGACCAGTTCATTCAAATTCTAAGTATCTAAAACAATT  
20   TTATAAAGCATTGCAAGGCTATGCCAAATCCAACGGTGTCTAGAAATTAAT  
AGTTGAGCCTTTTGATGATTACCAATTATTCAGTTCGGGAGTTCCTAGT  
AATCAGGGAAATGATAATCTGATTGAAGATTTTACCAGTTCAGGTTATCAC  
CATGATGGTTTAACAACCTGGTTTTACTGGTAAATATTTATCTTGGCACTATG  
TTAAAAATTTAGAAGGTGTCCTTCTGAAACGTTACTATCTTCATTCTCTAA  
GACAGGACGAGCTTTGGTTAAGAAAGCAATGTCTTTTGGAATCAAGGTTTC  
25   GCGTTCTTAAACGTGATGAGCTACATTTATTTAAAGAGATAACAACCTTCTA  
CGTCAAATAGACGTGATTATATGGATAAGTCCTTAGATTATTATCAAGATT  
TTTACGATAGCTTTGAAGGCAAGGCTGAATTTGTGATTGCCACTTTAAATT  
TTAGAGAATACGACCATAACTTGCAAATAAAAGCTGAAGCATTGGAAAAT  
AAGCTT

30

(SEQ ID NO: 192)  
MTLRELTIEEFKEHSGNYDSQSFLQTPEMAKLLEKRGYDVRYLGYQVENKLEI  
ISLSYIMPVTGGFQMKIDSGPVHSNSKYLKQFYKALQGYAKSNGVLELIVEPF  
DDYQLFTSSGVPSNQGNLIEDFTSSGYHHDGLTTGFTGKYLSWHYVKNLE  
35   GVTSETLLSSFSKTGRALVKKAMSFQIKVRVLKRDELHLFKEITTSTSNRRDY  
MDKSLDYYQDFYDSFEGKAEFVIATLNFREYDHNLQIKAEALENKL

40

Sequence description

- A) Length: 771 bp - 257 aa (partial gene sequence)  
B) This gene sequence was not identified using the LEEP system. It was  
identified immediately downstream of the ID-65 gene which was identified by

LEEP, during cloning and sequence analysis of the full-length ID-65 gene sequence. Sequence Characteristics:  
No obvious leader peptide sequence  
Orf is preceded by a potential Shine-Dalgarno sequence.

#### ID-174

Clone 2-17b (ID-80b)

(SEQ ID NO: 193)  
TTGTCATTAAGTTTGGTTGCAGTGTTAAATCTTATCCCTCCTAAAATCATGG  
GATCAGTTATTGATGCTATTACAACCTGGAAAATTAACAAGACCACAATTAC  
TATGGAATTTATTAGGTTTGGTTTTGTCAGCTTTAGCTATGTATGGGCTGCG  
TTATATTTGGCGTATGTATATTTTAGGGACTTCTTACAAATTAGGCCAAGTT  
GTCAGATACCGTTTATTTGAACATTTTACAAAAATGTCTCCTTCTTTTTATC  
AGAAATATCGTACAGGTGATTTAATGGCGCACGCGACCAACGACATCAAT  
TCTCTAACACGTCTTGCAGGAGGAGGAGTTATGTCAGCAGTGGATGCCTCT  
ATCACAGCATTAGTAACGCTTATCACCATGTTCTTTACTATTTTCGTGGCAA  
ATGACATTAATTGCGGTTATCCCTTTGCCCTTAATGGCCTTAGCACTAGTA  
AATTGGGGCGAAAAACCCATGAAACCTTCAAAGAATCTCAGGCAGCCCTT  
TTCAGAATTAAATAATAAAGTG  
(SEQ ID NO: 194)  
MSLSLVAVLNLIPPKIMGSVIDAITTGKLTRPQLLWNLLGLVLSALAMYGLRYI  
WRMYILGTSYKLGQVVRYRLFHFHTKMSPSFYQKYRTGDLMAHATNDINSLT  
RLAGGGVMSAVDASITALVTLITMFFTISWQMTLIAVIPLPLMALALVNWGEK  
PMKPSKNLRQPFSELNNKV

#### Sequence description

- A) Length: 534 bp - 178 aa (partial gene sequence)
- B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-80 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-80 gene sequence.
- Sequence Characteristics:
- No obvious leader peptide sequence  
Orf is preceded by a potential Shine-Dalgarno sequence.

ID-175

5 Clone 2-11Ab (ID-103b)

(SEQ ID NO: 195)  
ATGCATATTGAGACTGTTATTGATTTCAAAGAATTAGGAAAAAGATATCGT  
TTTAAAAATCCTACAAAAGAATTAATAGCTGATACTTTAGAACAAGTCTTA  
10 GAAGTGATAAAAGAAGTTGATTATTATCAATCTCAAATTATTATGTTGTT  
GGTTATTTATCTTATGAAGCATCTGCTGCTTTTGATTCACATTTTAAAGTTT  
CTCAACAGAAGTTGGCTGGAGAACATCTAGCTTATTTTACAGTACATAAAG  
ATTGTGAGAACGAAGCTTTTCCTTTAAGTTATGAAAATGTTAGATTAGCAG  
ATAATTGGACTGCTAATGTTTCTGAGCAAGAATATCAAGAGGCAATTGCTA  
15 ATATTAAAGGACAAATTAGACAAGGAAATACTTATCAAGTAAATTATACA  
CTAGAGCTTAGCCAACAATTATGCTCGGATCC

(SEQ ID NO: 196)  
MHETVIDFKELGKRYRFKNPTKELIADTLEQVLEVIKEVDYYQSQNYVVG  
20 LSYEASAAFD SHFKVSQQKLAGEHLAYFTVHKDCENEAFPLSYENVRLADNW  
TANVSEQEYQEALANIKGQIRQGNTYQVNYTLELSQQLCSD

Sequence description:

25 A] Length: 440 bp - 146 aa (partial gene sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-103 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-103 gene sequence.  
30 Shine Dalgarno sequence present upstream of  
ATG start codon, No apparent leader peptide sequence

ID-176

35

Clone 2-18/22b(b) (ID-104b)

(SEQ ID NO: 197)  
GTGAATAATATGTTTTATCTCAAAATAGCCTGGCATAATTTAAAACATTCT  
40 ATAGACCAGTACATAACCATTCTCTTAGCCAGTTTATTACTTTATTCATTGA  
CTTGTTCTACGCTACTAATCTTAATGAGTGCTGTTGGAAGAGATATGGGGA  
CAGCGGCAACGGTTCTTTTTCTTGGAGTGATTGTTTTGTCAATCTTTGCGGT  
AGTCATGGAACATTATAGCTACAATATCTTGATGAAACAGCGTAGTAGTG



AATTTGGACTGTATAACATTTTGGGGATGAATAAACGTCAAGTTGCGCGTG  
 TAGCTAGTCTAGAGCTGTTTATTATTTATATATTTCTTATTTCTATAGGAAG  
 TCTGTTTAGTGCTTTTTTTTGCTAAATTTATTTATTTAATTTTTGTCAACATTA  
 5 TTAACATCATGCCTAAATCTTAGTTTAAGTTTATGGCCATTTATTATTG  
 TATCGTTATATTTACAGGTATTTTCTGACTTTAGAAAGTTCCAGTTATTCGA  
 CATGTTTCATTTATCATCCCCATTAAGTCTTTTTAGAAAGAAACAACAGGGA  
 GAAAAAGAACCAAAAGGTAATCTTATACTTGCAATTTTAGCGTTAGTAGCT  
 ATCGCCATCGCTTATACAATGGCTCTTACTTCAGGTAAAGCACCTGCATTA  
 GCTGTTATCTATCGTTTCTTCTTTGCAGTACTTTTAGTAATTGCTGGTACTT  
 10 ATCTTTTTTATATTAGTTTTATGACATGGTACTTAAAAAGGTTGCGTCAAAA  
 CAAGCATTATTATTATAAATCTGAGCATTTTGTATCAACTTCGCAAATGAT  
 TTTTCGAATGAAGCAAAATGCAGTAGGGTTAGCAAGTATCACTTTATTAGC  
 TGTATGGCTCTAGTTACTATTGCTACAACAGTCTCACTCTATTCAAATACA  
 CAAAATGTTGTTACCGGACTATTTCCAAAATCAGTAAGTTTATCAATAGAT  
 15 AATTCAAAAGGTGACGCGAAAAATATATTTGAAGAAAAGATTTTGAAGAA  
 ACTAGGTAAGTCATCTAAGGAAGCTATCACTTATAATCAGACAATGATTC  
 GATGCCAGTTAGTCAATCAAGTGACTTAATATCACATCTA

20 (SEQ ID NO: 198)  
 MNNMFYLKIAWHNLKHSIDQYIPFLLASLLLYSLTCSTLLILMSAVGRDMGTA  
 ATVLFVLGVIVLSIFAVVMEHYSYNILMKQRSSEFGLYNILGMNKRQVARVASL  
 ELFIHYIFLISIGSLFSAFFAKFIYLFVNIINYHALNLSLSLWPFHICIVIFTGIFLTLE  
 VPVIRHVHLSSPLSLFRKKQQGEKEPKGNLILAILALVAIAIAYTMALTSGKAP  
 25 ALAVIYRFFFAVLLVIAGTYLFYISFMTWYLRRLRQNKHYYYKSEHFVSTSQM  
 IFRMKQNAVGLASITLLAVMALVTIATTVSLYSNTQNVVTGLFPKSVSLSIDNS  
 KGDAKNIFEKILKKLGKSSKEAITYNQTMISMPVVSQSSDLISHL

30

#### Sequence description:

- 35 A) Length: 1119 bp - 373 aa (partial gene sequence)  
 B) This gene sequence was not identified using the LEEP system. It was  
 identified upstream of the ID-104 gene which was identified by LEEP, during  
 cloning and sequence analysis of the full-length ID-104 gene sequence.  
 Possible Shine Dalgarno sequence present  
 40 upstream of a GTG start codon. Possesses a potential  
 leader peptide sequence

ID-177

Clone 2-5b (ID-112b)

(SEQ ID NO: 199)  
5 ATGGTTGAGCCAATTATTTCAATACAAGGACTTCATAAAAGTTTTGGGAAA  
AATGAGGTTTTAAAAGGCATTGACTTGGATATTCATCAAGGAGAAGTGGT  
GGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTAAAGAACAAT  
GAATCTCTTGGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGATTG  
10 ATATAACAGACAAAAAGAATGATATTTTTAAAATGCGCGAAAAAATGGGC  
ATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAT  
ATTACTTTATCACCTATTAAGACAAAGGGACTTTCTAAGCTTGATGCTCAG  
ACAAAAGCATACGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAA  
TGCTTATCCAGCAAGCTTATCTGGAGGACAACAACCGGATTGCTATTGC  
AAGAGGTCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAACCTACTTCA  
15 GCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTA  
GCTAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCA  
CGTGAAGTAGCGGATCGTGTCAATTATTATGGATGCAGGGATTATTGTTGAG  
CAAGGGACCCCTAAGAAAGTATTTGAGCAGACAAAAGAAATCCGCACAAG  
AGACTTCTTAAGTAAAGTATTATAA

20

(SEQ ID NO: 200)  
MVEPIISIQGLHKSFGKNEVLKGIIDLHQQGEVVVIIGPSGSGKSTFLRTMNLLE  
VPTKGTVTFEIDITDKKNDIFKMREKMGVMVFQQFNLFNMTVLENITLSPIKT  
KGLSKLDAQTKAYELLEKVGLKEKANAYPASLSGGQQQRIAIARGLAMNPDV  
25 LLFDEPTSALDPEMVGEVLTVMQDLAKSGMTMVIVTHEMGFAREVADRVIF  
MDAGIIVEQGTTPKKVFEQTKEIRTRDFLSKVL\*

30 Sequence description:

A] Length: 735 bp - 244 aa (full length gene)  
B] This gene sequence was not identified using the LEEP system. It was  
35 identified downstream of the ID-112 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-112 gene sequence.  
Shine-Dalgarno sequence precedes the 'ATG'  
start codon. No obvious leader peptide

40 ID-178

Clone 2-5c (ID-112c)

(SEQ ID NO: 201)

ATGTCTCAsTATCAAGAGTGGTTAGAAAACGACTCACTCGGTAAAGATATT  
AAGTCAGATTTAGAAGCTATTAAGGAGATGAATCTGAAATTCAGGATCG  
TTTTTACAAAACATTAGAATTTGGAACGGCGGGATTGAGAGGTAAACTTG  
GAGCAGGAACCAATCGTATGAATACTTATATGGTGGGGAAAGCAGCACAA  
GCATTAGCTAATCGATTATTGATCATGGCCCTGAAGCTATTGCACGTGGAA  
TTGCAGTTAGTTATGATGTCCCGTTATCAATCTAAGGAATTTGCAGAATTA  
ACTTGGTCCATTATGGCAGCAAATGGTATTAAAGCCTTATATTTA

(SEQ ID NO: 202)

MSHMNYKEIYQEWLENDLGLGKDIKSDLEAIKGDESEIQDRFYKTLEFGTAGLR  
GKLGAGTNRMTYMGVKGAAQALANRLLIMALKLLHVELQLVMMSRYQSKE  
FAELTWSIMAANGIKALYL

Sequence description:

A] Length: 366 bp - 122 aa (partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-112 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence preceded the 'ATG' start codon. No obvious potential leader peptide sequence.

ID-179

Clone 2-5d (ID-112d)

(SEQ ID NO: 203)

ATGCAACCTGTAAAAGTCGATGAACCTTCTGTTGAAGAAACCATTACTATT  
TTGAAAGGTATCCAAAAAATAACGAAGATTATCATCACGTAAAATATAA  
TAATGATGCCATAGAAGCAGCTGCAGTACTATCTAATCGTTATATCCAAGA  
CCGCTTTTTACCTGATAAAGCAATAGACTTATTAGATGAAGCTGGTTCTAA  
AATGAACCTAACACTAAATTTTGTGATCCAAAAGAAATTGATCAACGTCT  
CATTGAAGCAGAAAATTTAAAAGCGCAAGCGACTCGTGAAGAAGATTACG  
AACGTGCAGCTTACTTCCGTGACCAGATTGCAAAATATAAAGAAATGCAG  
CAACAAAAGGTCGACGATCAAGATACACCTATTATTACCGAAAAACAAT  
TGAGCACATCATTGAAGAAAAAACGAATATCCCTGTTGGTGATTTAAAAG  
AAAAAGAACAACTCTCAATTAATTAATCTCGCAGATGACTTGAAACAGCAT  
GTGATCGGCCAGGATGACGCTGTCATTAAGATTGCAAAAGCTATTCGTCGT  
AATCGAGTTGGTCTTGGTAGCCCAAACCGTCCTATTGGTTCCTTTTTATFTG  
TAGGACCAACCGGTGTTGGTAAAACTGAACTTTCTAAACAACTAGCAATTG  
AGCTCTTTGGTTCAGCTGATAGTATGATTCGTTTTGATATGTCAGAGTACAT  
GGAAAAGCATGCTGTTGCTAAATTAGTCGGAGCGCCTCCAGGATACGTGG  
GATACGAGGAAGCTGGACAATACTGAAAAGGTTTCGTCGAAATCCTTAC  
TCGCTCATCCTTCTAGATGAAATTGAAAAAGCTCATCCCGATGTCATGCAT

5 ATGTTCTTGCAGGTCCTTGATGACGGTCGATTAACAGATGGACAAGGAAG  
AACTGTTAGTTTTAAAGATAACCATTATCATCATGACCTCAAATGCTGGTTC  
TGGTAAAACTGAAGCAAGTGTGGCTTTGGTGCCTCACGAGAAGGTAGGA  
CGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCAT  
GCAAGC

(SEQ ID NO: 204)  
10 MQPVKVDEPSVEETITILKGIQKKYEDYHHVKYNNDAIEAAVLSNRYIQDRF  
LPDKAIDLLDEAGSKMNLTLNFVDPKEIDQRLIEAENLKAQATREEDYERAAY  
FRDQIAKYKEMQQQKVDDQDTPITEKTIEHIEEKTNPVVDLKEKEQSQLINL  
ADDLKQHVIGQDDAVIKIAKAIRNRVGLGSPNRPISFLVVGPTGVGKTELSK  
QLAIELFGSADSMIRFDMSEYMEKHAVAKLVGAPPGYVGYEEAGQLTEKVRR  
NPYSLILLDEIEKAHPDVMHMFLLQVLDDGRLTDGQGRTVSFKDTIIMTSNAGS  
GKTEASVGFASREGRTNSSSVPGDPLESTCRHAS

15

#### Sequence description:

20

A) Length: 1070 bp ÷ 356 aa (Partial gene sequence)

25

B) This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-112 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-Dalgarno sequence preceded the 'ATG' start codon. No obvious potential leader peptide sequence.

ID-180

30

Clone 2-7b (ID-113b)

(SEQ ID NO: 205)  
35 ATGAGAGGGAAGGTTATTTACGGCACAACCCTTATAGGTCTTTTTCTATTC  
TTATTTTTCTATTTTTGGATTCTTAAGCATCACATCGAGAGAATACATCATC  
ATCGTATAAAGCAGGTAGATGCGAAGAGTGATTTAACAGGATTAAAACC  
CATTTGCCCATTCAGCATTGATACAAAGCAACAAGTTATTCCTCTTGTT  
ACAAAAGAAGGCGGAAAATATGTCAAAGCTAGGGATAATATTAATGTTGA  
TATCGAATTACGGGATTCTCCAAGTAGATCACATCATTCAGAAAAGCC  
40 GAGAATTAGGACAAAAGGGTTAATATCATATAGAGGAAATTCCTCTCGTT  
ACTTTGATAAGAAGTCATTGAAAGTTAAGTTTGTTACTAATAAGTTAAAGG  
AAAAGAAGCATCGATTAGCAGGAATGCCTAAAGAATCGGAGTGGGTATTG  
CATGGTCCCTTTCTAGACAGAACATTATTAAGAAATTATCTGAGTTATAAT

ATTGCTGGTGAGATTATGCCTATGCCCCAAACGTTTCGCTACTGTGAGTTAT  
TTGTCAATGGTGAGTATCAGGGAG

(SEQ ID NO: 206)

5 MRGKVIYGTTLIGLFLFLFFYFWIPKHHIERIHHRKQVDAKSDLTGFKTHLP  
SIDTKQQVIPLVTKEGGKYVKARDNINVDIELRDSPSRSHLSEKPRIRTKGLIS  
YRGNSSRYFDKKSLLKVKFVTNKLKEKKHRLAGMPKESEWVLHGPFLDRTLLR  
NYLSYNIAGEIMPMPQTFATVSYLSMVSIRE

10

Sequence description:

A] Length: 582 bp - 194 aa (Partial gene sequence)

15 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-113 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-113 gene sequence.  
ATG start codon is preceded by a Shine-  
Dalgarno sequence-Possesses a potential leader peptide  
sequence. C-terminus to be determined.

20

ID-181

25

Clone 2-17b (ID-117b)

(SEQ ID NO: 207)

30 CTTACATTTTATTGATCACTATCTGACAAATGTTAATCAAACAGCAGTTCT  
TATTTTAGTGGGATATTATTCAATGTATGTCTTGCAGACCTTAATTCAATAT  
TTTGGGAATCTCTTTTTTGC GCGTGTCTTATAGTATTGTTAGAGATATTC  
GTAGAGATGCTTTTGCTAATATGGAAAGGCTAGGCATGTCTTATTTTGATA  
GGACACCGGCAGGATCTATTGTGTACGTATTACTAATGATACTGAAGCAA  
TATCTGATATGTTTTCGGGTATTTTATCAAGTTTTATCTCGGCGATATTTAT  
35 TTTTACAGTTACTCTGTACACTATGTTGATGCTAGACATTAACTAACAGG  
ACTCGTCGCTCTTTTGTTACCTGTTATCTTTATATTAGTGAATGTCTATCGG  
AAAAAATCAGTCACTGTCATTGCTAAAACGAGAAGTTTACTTAGTGATATC  
AACAGTAAATTATCAGAAAGTATTGAAGGAATTC

40 (SEQ ID NO: 208)

SHFIDHYLTNVNQTAVLILVGYYSMYVLQTLIQYFGNLFFARVSYSIVRDIRRD  
AFANMERLGMSYFDRTPAGSIVSRITNDTEAISDMFSGILSSFISAIFIFTVTLYT  
MLMLDIKLTGLVALLLPVIFILVNVYRKKSVTVIKTRSLSDINSKLSEIEGI

Sequence description:

A] Length: 498 bp - 165 aa (Partial gene sequence)

5 B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-117 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-117 gene sequence. N- and C-termini have yet to be determined

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ID-182

15

Clone 3-8b (ID-120b)

(SEQ ID NO: 209)  
20 ATGTACCATATTGAATTAAAAAAGGAAGCTTTACTACCAAGAGAACGCCT  
AGTTGATTTAGGCGCAGATAGATTGAGTAATCAGGAGTTATTAGCCATTCT  
CTTACGTACAGGTATTAAAGAAAAACCTGTTCTTGAAATTTCAACGCAAAT  
TTAGAAAACATAAGCAGTTTAGCAGATTTTGGTCAATTATCCTTACAGGA  
GTTGCAATCCATTAAAGGAATCGGTCAGGTTAAATCCGTCGAAATAAAAG  
CTATGCTAGAACTAGCAAAACGGATTCACAAAGCTGAATATGATCGTAAA  
25 GAGCAAATTTTAAAGTAGTGAACAATTAGCGAGGAAAATGATGCTCGAATT  
AGGGGATAAAAAACAAGAACATTTAGTAGCTATTTATATGGATACACAAA  
ATCGTATTATCGAACAGAGAACTATTTTTATTGGTACTGTACGTCGTTTCAG  
TAGCAGAGCCAAGAGAAATTCTACATTATGCTTGTA AAAACATGGCAACT  
TCTTTGATTATTATACATAATCATCCCTCAGGTTCTCCAAATCCCAGTGAAA  
30 GTGATTTAAGTTTCACTAAAAAAATAAAACGATCATGTGATCATCTGGGAA  
TTGTCTGCCTAGATCACATCATCGTTGGAAAAAATAAATATTATAGTTTTC  
GAGAAGAAGCAGATATTTTATAA

(SEQ ID NO: 210)  
35 MYHIELKKEALLPRERLVDLGADRLSNQELLAILLRTGIKEKPVLEISTQILENI  
SSLADFGQLSLQELQSIKGIGQVKSVEIKAMLELAKRIHKA EYDRKEQILSSEQ  
LARKMMLELGDKKQEH LVAIYMDTQNRIIEQRTIFIGTVRRSVAEPREILHYAC  
KNMATSLIIHNHPSGSPNPSES DLSFTKKIKRSCDHLGIVCLDHIIVGKNKYYSF  
READIL\*

40

Sequence description:

A] Length: 681 bp - 227 aa (full-length gene)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-120 gene which was identified by LEEP,

during cloning and sequence analysis of the full-length ID-120 gene sequence.  
ATG start codon is preceded by an typical  
Shine-Dalgarno sequence. No obvious leader  
peptide sequence

5

ID-183

10

Clone 3-11b (ID-121b)

(SEQ ID NO: 211)  
15 TGGTTAAAAGTAGTGATAGCTTGTATTCCATCTATTTTAATTGCTTTACCAT  
TTGATAATTGGTTTGAAGCTCATTTTAATTTTCATGATTCCGATTGCAATAGC  
CCTAATCTTTTATGGTTTTGTCTTCATATGGGTTGAAAAACGTAATGCACAC  
CTCAAACCACAGGTAACCGAATTGGCAAGTATGTCTTACAAGACAGCTTTC  
TTGATTGGATGTTTCCAGGTTCTCAGTATTGTTCCGGGAACCAGTCGTTCTG  
GAGCTACTATTTTAGGAGCAATTATTATTGGAAGTAGTCGTTCCGGTCGCTG  
20 CTGACTTTACTTTCTTCCTTGCCATCCCAACTATGTTTGGTTATAGTGGACT  
TAAGGCGGTAAATATTTTTTAGATGGTAACGTCTTGAGTTTAGACCAATC  
TTTAATACTTTTAGTAGCAAGTCTGACAGCTTTCGTAGTTAGTTTATATGTT  
ATTCGTTTCTTGACAGACTATGTCAAACGACACGATTTCACCATCTTTGGT  
AAGTATCGTATAGTCTTAGGAAGTTTACTCATCCTCTACTGGTTAGTTGTTC  
25 ATTTATTCTAA

(SEQ ID NO: 212)  
30 WLKVVIACIPSILIALPFDNWFEAHFNFMIPIALIFYG FVFIWVEKRNAHLKP  
QVTELASMSYKTAFLIGCFQVLSIVPGTSRSGATILGAIIGTSRSVAADFTFFLA  
IPTMFGYSGLKAVKYFLDGNVLSLDQSLILLVASLTAFFVVS LYVIRFLTDYVKR  
HDFTIFGKYRIVLGSLLILYWL VVHLF\*

Sequence description:

35 A] Length: 579 bp - 193 aa (partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-68 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-68 gene sequence  
described in WO 00/06736. N-terminus has yet to be determined.

40

ID-184

Clone 3-11c (ID-121c)

(SEQ ID NO: 213)  
ATGGAAATGAAACAAATCAGTGAAACAACACTGAAAATTACAATTAGTAT  
5 GGAAGATTTAGAAAGATCGTGGTATGGAGCTGAAAGATTTCCCTAATCCCTCA  
GGAGAAGACTGAGGAATTTTTCTATTCTGTCATGGATGAATTAGACTTGCC  
AGAAAACCTTTAAAAATAGTGGTATGTTAAGTTTTTCGAGTAACACCTAAAA  
AAGATCGCATTGATGTTTTTGTACAAAGTCTGAATTAAGTAAAGATTTAA  
ATTTAGAAGAATTAGCAGATTTGGGTGACATTTCAAAAATGTCTCCAGAAG  
10 ACTTTTTTAAAACCTTGGAACAATCGATGTTGGAAAAAGGGGATACGGAT  
GCCCATGCCAAATTAGCAGAAATTGAAAATATGATGGATAAAGCAACTCA  
AGAAGTAGTTGAGGAAAATGTTTCTGAAGAACAACCTGAAAAGGAAGTAG  
AAACGATTGGATATGTTCACTATGTCTTTGATTTTGATAATATTGAAGCTGT  
AGTTCGATTTTCACAAACGATTGATTTTCCAATAGAAGCTT

(SEQ ID NO: 214)  
15 MEMKQISETTLKITISMEDLEDRGMELKDFLIPQEKTEEFFYSVMDELDLPENF  
KNSGMLSFRVTPKKDRIDVFVTKSELSKDLNLEELADLGDISKMSPEDFFKTLE  
QSMLEKGD TDAHAKLAEIENMMDKATQEVVEENVSEEQPEKEVETIGYVHY  
VFDFDNIEAVVRFSQTIDFPIEA

20

Sequence description:

A] Length: 547 bp - 182 aa (Partial sequence)  
25 B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-68 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-68 gene sequence.  
ATG start codon is preceded by an typical  
Shine-Dalgarno sequence. No obvious potential  
30 leader peptide  
sequence

35 ID-185

Clone 3-16b (ID-122b)

(SEQ ID NO: 215)  
40 GGAAACCAACGGCCAGTACAATCGTCAAGGGTAGATTATCCTAAACGTAG  
TCGTGCCAAGATTGTAGAAGTTTATTTTAGACAAGCTTCTACTACTGATTA  
TTCTGGTGTTTACAAAGGTTACTATATTGACTTTGAAGCCAAAGAAACCCG  
GCAGAAAACCTGCTATGCCTATGAAAAATTTTCATGCTCACCAAATAGAGC  
ACATGGCAAATGTATTACAGCAAAAAGGGATTGCTTTGTCTTGCTTCATT



TTTCCACACTTAAGGAAACCTATCTACTCCCTGCTAATGAGTTAATTTTCATT  
TTATCAGATTGATAAAGGCAATAAATCAATGCCTATTGATTATATCAGAAA  
AAATGGATTTTTCGTAAAGGAGAGTGCCTTTCCTCAAGTCCCTTACTTAGA  
TATTATTGAAGAAAAATTATTAGGCGGTGATTACAATTAA

5

(SEQ ID NO: 216)

GNQRPVQSSRVDYPKRSRAKIVEVYFRQASTTDYSGVYKGYIDFEAKETRQ  
KTAMPMKNFHAHQIEHMANVLQQKGICFVLLHFSTLKETYLLPANELISFYQI  
DKGNKSMPIDYIRKNGFFVKESAFPQVPYLDIIEEKLLGGDYN\*

10

Sequence description:

A] Length: 447 bp - 149 aa (partial sequence)

15

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-122 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-122 gene sequence. N-terminus has yet to be determined

20

ID-186

Clone 3-17b (ID-123b)

25

(SEQ ID NO: 217)

GGATCCTAAAAACGCTAAGGTTTATCAAAAAAATGCTGATCAATTTAGTG  
ACAAGGCAATGGCTATTGCAGAGAAGTATAAGCCAAAATTTAAAGCTGCA  
AAGTCTAAATACTTTGTGACTTCACATACAGCATTCTCATACTTAGCTAAG  
30 CGATACGGATTGACTCAGTTAGGTATTGCAGGTGTCTCAACCGAGCAAGA  
ACCTAGTGCTAAAAAATTAGCCGAAATTCAGGAGTTTGTGAAAACATATA  
AGGTTAAGACTATTTTTGTTGAAGAAGGAGTCTCACCTAAATTAGCTCAAG  
CAGTAGCTTCAGCTACTCGAGTTAAAATTGCAAGTTTAAGTCCTTTAGAAG  
CAGTTCCCAAAAACAATAAAGATTACTTAGAAAATTTGGAAACTAATCTTA  
35 AGGTACTTGTCAAATCGTTAAATCAATAG

35

(SEQ ID NO: 218)

DPKNAKVYQKNADQFSDKAMAIAEKYKPKFKAASKYFVTSHTAFSYLAKR  
YGLTQLGIAGVSTEQEPSAKKLAEIQEFVKTYKVKTIFVEEGVSPKLAQAVAS  
40 ATRVKIASLSPLEAVPKNNKDYLENLETNLKVLVKS LNQ\*

40

Sequence description:

A] Length: 433 bp - 144 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-123 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-123 gene sequence. N-terminus has yet to be determined

ID-187

Clone 3-46/47 (ID-130b)

(SEQ ID NO: 219)

ATGAAAAAAGTCATCGATTAAAAAACTACAAAAAGCATACGCCTCAGA  
AACTGTTTTAAATAATATTAATTTGGAGGTGTTTAAAGGAGAAATAATTGG  
ATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTAAAACTATGCT  
TGGCATGGAAAAAGCAGATAAGGGAACAGCTCTTGTTCTTGATACTCAAA  
TGCCAGATCGTAATATTTTAAATCAAATTGGCTATATGGCTCAATCTGATG  
CCTTACACGAGTCTTTAACTGGCTTAGAAAATTTATTATTCTTTGGAAAAA  
TGAAAGGTATTCAAAAAACTGAATTAACAGCAGATAACTCATATTTCT  
AAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCA  
GAAGGTATGAAAAGACGGCTTCTCTAGCCATCGCCCTACTTGGAACCCC  
ACAGTTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGG  
AGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGGACGTTCTAT  
CTTTATTACAACCCACGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGC  
ACTACTATTACGTGGAAACATTATTGCCTTTGATACTCCATTACATTTAAA  
AAAACAATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGG  
AGAATAA

(SEQ ID NO: 220)

MKKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKTMLGME  
KADKGTALVLDTPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQ  
KTELKQQITHISKVVDLENQLDKFVSGYSEGMKRRLSLAIALLGNPVLLDEP  
TVGIDPSLRRKIWQELINIKDEGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTP  
LHLKKQFNVSTIEEVFLKAEGE\*

Sequence description:

A] Length: 717 bp - 239 aa (Possible full-length sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-130 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-130 gene sequence. ATG start codon is preceded by a possible

Shine-Dalgarno. No obvious potential leader  
peptide sequence

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ID-188

Clone 3-83b (ID-144b)

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(SEQ ID NO: 221)  
ATGGGTACAAATGATACATGATATGATTAACAATTGAGCATTTTGCTGAG  
ACACAAGCTGATTTTCCAGTGTATGATATTTTAGGGGAAGTCCATACTTAT  
GGACAACCTTAAAGTAGACTCTGACTCTCTAGCTGCTCATATTGATAGCCTA  
GGCCTTGTTGAAAAATCACCTGTCTTAGTATTCGGTGGTCAAGAATATGAA  
15 ATGTTGGCGACATTTGTTGCTTTAACAAAGTCAGGGCATGCTTATATACCG  
GTTGACCAACACTCTGCTTTGGATAGAATACAGGCTATTATGACAGTTGCT  
CAACCAAGCCTTATCATTTC AATTGGTGAATTCCTCTTGAAGTTGATAAT  
GTCCCAATCCTAGACGTTTCTCAAGTTTCAGCTATTTTTGAAGAAAAGACT  
CCTTATGAGGTAACACATTCTGTAAAGGTGATGATAATTACTATATTATT  
20 TTCCTTCAGGGACTACTGGTTTACCAAAAGGTGTGCAAATTTACATGAC  
AATTTATTGAGCTTTACAAATTGGATGATTTCTGATGATGAGTTTTTCAGTTC  
CTGAAAGACCGCAAATGTTGGCTCAACCC

25

(SEQ ID NO: 222)  
MVQMIHDMIKTIEHFAETQADFPVYDILGEVHTYQQLKVDSDSLAAHIDSLGL  
VEKSPVLVFGGQYEYEMLATFVALTKSGHAYIPVDQHSALDRIQAIMTVAQPSL  
IISIGEPLEVDNVPILDVSVQVSAIFEEKTPYEVTHSVKGDDNYIIFTSGTTGLP  
KGVQISHDNLLSFTNWMISDDEFSVPERPQMLAQP

30

Sequence description:

35

A] Length: 592 bp - 197 aa (partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-144 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-144 gene sequence.  
Putative ATG start codon is preceded by a  
typical Shine-Dalgarno sequence. No obvious  
leader peptide sequence

40

This orf is not in frame with nuc

ID-189

Clone 3-86b (ID-145b)

5 (SEQ ID NO: 223)  
ATGGAAAATCATCGTTATGAAGATGAAGGTAAATTCCAGCGTAAGATGAC  
CAGTCGTCATCTCTTTATGTTATCGCTAGGTGGTGTATCGGGACTGGGCTT  
TTCTTGAGTTCAGGTTATACCATTGCACAGGCTGGTCCGCTTGGAGCTGTG  
CTGTCTTATTTGATTGGTGCCGTTGTGGTTTATTTGGTCATGCTATCACTTG  
10 GGGAATTGGCGGTTGCCATGCCGGTGACGGGGTCATTCCACACTTATGCCA  
CTAAGTTTATCAGTCCTGGAACAGGTTTTACTGTTGCTTGGCTATATTGGAT  
TTGTTGGACGGTCGCCTTGGGGACTGAATTTTAGGTGCTGCCATGCTGAT  
GCAGCGCTGGTTCCCAAATGTGCCGGCTTGGGCATTTGCTTCCTTTTTTGGC  
CTTGTGATTTTTGGTTTAAATGCTCTTAGCGTACGCTTTTTTGCAGAAGCAG  
15 AGTCTTTCTTCTCAAGTATTAAGGTATTGCTATCATTATCTTTATTATCTTG  
GGCTTAGGTGCTATGTTTGGTCTAGTTTCCTTTGAAGGTCAGCACAAAGGCT  
ATTCTCTTCACTCATCTGACTGCCAATGGTGCCTTTCCAAATGGTATCGTTG  
CAGTTGTCTCAGTCATGTTGGCTGTAACTATGCCTTCTCTGGTACTGAGTT  
AATTGGTATTGCGGCTGGTGAAACGGATAATCCCAAAGAAGCTGTACCAA  
20 GGGCTATTAAAACGACAATCGGTCGCTTGGTTGTTTTCTTTGTACTGACAA  
TTGTTGTCCTAGCTTCGCTATTGCCAATGAAAGAGGCAGGCGTATCCACAG  
CACCATTTCGTTGATGTCTTTGACAAGATGGGAATCCCTTTTACGGCGGATA  
TCATGAACTTCGTTATCTTGACAGCCATCCTGTCTGCTGGTAACTCAGGTCT  
CTACGCATCAAGCCGTATGCTCTGGTCCCTTGCCAATGAAGGTATGTTGTC  
25 AAAATCTGTTGTGAAAATCAATAAACACGGTGTCCCAATGCGTGCTCTTCT  
CTTGTCAATGGCAGGAGCAGTGCTGTGCGCTCTTTTCAAGTATTTACGCTGC  
AGACACAGTTTATCTAGCCTTGGTTTCAATCGCGGGCTTTGCTGTTGTTGTC  
GTATGGCTAGCCATTCCAGTCGCACAAATCAATTTCCGCAAGGAATTC  
30 (SEQ ID NO: 224)  
MENHRYEDEGKFQRKMTSRHLFMLS LGGVIGTGLFLSSGYTIAQAGPLGAVL  
SYLIGAVVVYLVMLS LGELAVAMPVTGSFHTYATKFISPGTGFTVAWLYWIC  
WTV ALGTEFLGAAML MQRWFPNVP AWAFASFFALVIFGLNALS VRFFAEAES  
FFSSIKVIAIIIFILGLGAMFGLVSFEGQHKAILFTHLTANGAFPNGIVAVV SVM  
LAVNYAFSGTELIGIAAGETDNPKEAVPRAIKTTIGRLV VFFVLTIVVLASLLPM  
35 KEAGVSTAPFVDVFDKMGIPFTADIMNFVILTAILSAGNSGLYASSRMLWSLA  
NEGMLS KSVVKINKHGVP MRALLLSMAGAVLSLFSSIIYAADTVYLALVSIAGF  
AVVVVWLAIPVAQINFRKEF

40

Sequence description:

A] Length: 1126 bp - 393 aa (partial gene

sequence)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-145 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-145 gene sequence.

Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possesses a possible leader peptide sequence.

ID-190

Clone 3-94b

(SEQ ID NO: 225)  
TCAGAAAATGCAGAGGCAGCAACGGTTGCCACAACTTGGTTACCAAAGG  
AGCTAATGTCATTATCGGACCAGCAACATCGGGTGCAGCTGCATCTTCAAC  
TCCAAAAGTAAATGCAGCAGCAGTTCCAATGATTGCACCTGCTGCGACAC  
AAGACAATTTAGTCTATGGTTCTGATGGAAAAACCTTAAATCAGTATTTCT  
TCCGAGCTACTTTTGTCTGATAATTATCAAGGAAAGCTATTGTCTCAGTATG  
CTACAGACAACCTTAAAGCTAAAAAAGTTGTTCTATTTTATGATAATTCAT  
CAGATTACTCAAAGGGGGTAGCAAAATCATTTAAGGAAAGTTATAGTGGA  
AAAATTGTTGATAGTATGACATTCTCCGCTGGTGATACTGATTTCCAAGCG  
TCATTGACTAAGTTGAAAGGGAAAGAATATGATGCTATTGTGATGCCAGG  
TTACTATACCGAGACAGGATTAATAGTTAAGCAAGCGCGTGATTTAGGTAT  
CTCTAAACCGGTTCTTGGGCCTGATGGTTTTGATAGTCCGAAATTTGTGCA  
ATCGGCAACACCTGTAGGAGCTTCAAACGTTTATTATTTGACAGGTTTCAC  
TACACAAGGATCAACCAAAGCTAAAGCT

(SEQ ID NO: 226)  
SENAEAAATVATNLVTKGANVIIGPATSGAAASSTPKVNAAA VPMIAPAATQD  
NLVYGSDGKTLNQYFFRATFVDNYQGKLLSQYATDNLKAKKVVLFDNSSD  
YSKGVAKSFKESYSGKIVDSMTFSAGD TDFQASLTKLKGKEYDAIVMPGYT  
ETGLIVKQARDLGISKPVLGPDGFDSPKFVQSATPVGASNVYYLTGFTTQGST  
KAKA

Sequence description

A] Length: 637 bp - 231 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-149 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-149 gene sequence. N- and C-termini have yet to be determined

5

#### ID-191

10

Clone 2-c94b (ID-153b)

(SEQ ID NO: 227)  
15 TTGGGACTTAAAGACCATGCTTTAGTCTATCCATTTTCATTATCTGGGGGG  
CAAAAGCAACGTGTCGCACTAGCTCGTGCGATGATGATTGATCCACAGATT  
ATTGGTTATGATGAGCCAACTAGCGCTCTTGATCCAGAGTTGCGTCAAGAA  
GTAGAAAACTAATTTTACAAAATAGAGAAACAGGTATGACACAAATTGT  
AGTAACACATGATCTTCAATTTGCTGAAAGTATATCTGATACGATTCTCAA  
AATTAATCCTAAGTAG  
20 (SEQ ID NO: 228)  
MGLKDHALVYPFSLSGGQKQRVALARAMMIDPQIIGYDEPTSALDPELRQEV  
EKLILQNRETGMTQIVVTHDLQFAESISDTILKINPK\*

25

Sequence description

30 A] Length: 270 bp - 90 aa (partial sequence)  
B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-153 gene which was identified by LEEP, during cloning and sequence analysis of the ID-153 gene sequence.  
N-terminus has yet to be determined

35

#### ID-192

Clone 2-c1b (ID-155b)

40

(SEQ ID NO: 229)  
ATGACTAATATCTCAGATGTTCCAAAAGCTATTAGAACACAGGCACAGTAT  
GTTCTCTTGGGAATGAGAGTTATGGATCAGTCGGTATTACCGAAAACATAT  
AATTCAAAAGAACCTTATTTGAAACCAGATATGATTTATATTCATGATAGA

AGACAAGAGACAATGCTTAAAATCACTCAAGAAATAGAAATGGAGCATTG  
A

(SEQ ID NO: 230)

MTNISDVPKAIRTQAQYVLLGMRVMDQSVLPKTYNSKEPYLKPDMIYIHDRR  
QETMLKITQEIMEH\*

#### Sequence description

A] Length: 204 bp - 68 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-155 gene which was identified by LEEP, during cloning and sequence analysis of the ID-155 gene sequence.

ATG start codon is preceded by a potential typical Shine-Dalgarno sequence.

Has a  
typical leader peptide. N-terminus has yet to be  
verified

#### ID-193

Clone 2-54altb (ID-172b)

(SEQ ID NO: 231)

AAGCTTGCATGCCTGCAGGTCGACTCTAGAGGATCTTGGGGAATATAAATT  
TGGATTTTCATGACGATGTAAAGCCAATTTATTCTACGGGAAAAGGTCTAAA  
TGAGGCTGTTATTCGTGAGTTATCTGCAGCTAAGGGTGAACCTGAGTGGAT  
GTTGGACTTTCGTCTAAAATCCTTGGAAACGTTTAATAAAATGCCGATGCA  
GACCTGGGGAGCAGATTTATCAGATATTGATTTTGATGATATTATTTATTA  
TCAAAAAGCATCTGATAAACCTGCGCGTGATTGGGATGATGTTCCAGAAA  
AAATCAAAGAACTTTTGAAAGAATTGGGATTCCAGAAGCTGAAAGAGCC  
TATCTTGCAGGAGCATCAGCACAAATATGAATCAGAAGTAGTTTATCACAAT  
ATGAAAGAAGAATATGATAAGCTGGGTATTGTTTTTACGGATACTGACTCT  
GCACTTAAAGAGTACCCAGAGCTATTCAAAAAATATTTTGCTAAACTTGTC  
CCTCCAACAGATAATAAATTAGCTGCTCTGAACTCTGCTGTATGGTCAGGT  
GGAACATTTATTTATGTTCCCTAAAGGTGTTAAGGTGGATATTCCACTTCAA  
ACTTACTTCCGTATTAATAATGAAAATACTGGACAATTTGAACGTAATCTC  
ATTATTGTTGATGAGGGAGCAAGTGTTCACTATGTTGAAGGTTGTACCGCC  
CCAATTATTCTTCAAATAGTTTACATGCAGCTATAGTTGAAATTTTTGCAC  
TTGATGGAGCTTATATGCGCTATACGACTATTCAAAATTGGTCCGATAATG  
TCTATAATTTAGTGACAAAACGTGCTACCGCTAAAAAAGATGCAACAGTT  
GAGTGGATAGATGGAAATCTAGGAGCTAAAACAACAATGAAATACCCATC

GGTTTACCTTGATGGTGAAGGAGCACGTGGCACGATGTTGTCTATTGCTTT  
TGCAAACAAAGGACAACACCAAGATACGGGTGCAAAGATGATTCATAATG  
CCCCCATACTAGTTCATCCATTGTCTCTAAATCAATTGCTAAGGGTGGGG  
GAAAAGTTGATTATCGAGGTCAAGTGACATTTAATAAAGATTCCAAAAAA  
5 TCAGTGTACATATAGAATGTGACACCATATTGATGGATGATATTTCAAAA  
TCAGATACCATAACCGTTTAATGAGATTCATAATTCACAGGTTGCTTTAGAG  
CATGAAGCAAAGGTGTCTAAGATTTCTGAAGAGCAACTGTACTACTTGATG  
AGTCGAGGTTTATCTGAAGCTGAAGCAACAGAAATGATTGTTATGGGGTTT  
GTTGAGCCCTTTACGAAAGAATTACCAATGGAATATGCGGTAGAGTTAAA  
10 TCGTTTAATTCCTATGAAATGGAAGGTTTCAGTTGGTTAA

(SEQ ID NO: 232)  
MHACRSTLEDLGEYKFGFHDDVKPIYSTGKGLNEAVIRELSAAKGEPEWMLD  
FRLKSLETFNKMPMQTWGADLSIDFDDIYYQKASDKPARDWDDVPEKIKE  
15 TFERIGIPEAERAYLAGASAQYESEVVYHNMKEEYDKLGIVFTDSDSALKEYP  
ELFKKYFAKLVPPTDNKLAALNSAVWSGGTFIYVPKGVKVDIPLQTYFRINNE  
NTGQFERTLIIVDEGASVHYVEGCTAPTYSSNSLHAAIVEIFALDGAYMRYTTI  
QNWSDNVYNLVTKRATAKKDATVEWIDGNLGAKTTMKYPSVYLDGEGARG  
TMLSIAFANKGQHQDTGAKMIHNAPHTSSSIVSKSIKGGGKVDYRGQVTFN  
20 KDSKKSVMHIECDTILMDDISKSDTIPFNEIHNSQVALEHEAKVSKISEEQLYYL  
MSRGLSEAEATEMIVMGFVEPFTKELPMEYAVELNRLISYEMEGSVG\*

Sequence description:

25 A] Length: 1411 bp - 469 aa (Possible full-length gene)  
B] This gene sequence was not identified using the LEEP system. It was  
identified downstream of the ID-72 gene which was identified by LEEP,  
during cloning and sequence analysis of the full-length ID-72 gene sequence.  
30 No obvious Shine Dalgarno sequence upstream of  
TTG start codon (insufficient sequence data). N  
terminus needs verification.

35 ID-194

Clone 3-1b (ID-81b)

(SEQ ID NO: 233)  
40 ATGATAGAATTCTTTTCTAATATCAGAACAGAGATTCCGCAGATGCCTTTA  
CTTATCCATAGTTTGATTTTATCTGTCTTACCTTTTCTGATGTGGCTGACTTT  
GGTTAATAGAGATAAGCCTTTGTATAAACTATTTGGAGTATCCTTTTAGG  
ACTTCAGTTAATTACGATTTATACTTGGTTTTTCTGGGCAAATTGCCTTTA



TCTGAAAGTCTTCCCCTTTACCATTGTCGAATAGGCATGTTTGTCTGGTCTCT  
TA

(SEQ ID NO: 234)

MIEFFSNIRTEIPQMPLLIHSLILSVLPFLMWLTLVNRDKPLYKTIWSILLGLQLI  
TIYTWFFWAKLPLSESLPLYHCRIGMFVGLL

Sequence description

A) Length: 261 bp - 87 aa (partial gene sequence)

B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-81 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-81 gene sequence. Sequence Characteristics: Possesses a potential leader peptide sequence. Orf is preceded by a potential Shine-Dalgarno sequence.

ID-195

Clone RS-55b

(SEQ ID NO: 235)

AAGCTTGTGCAAAGTATTAAAGAGATAGGATTAGCTAATGCGCATTATTATTA  
GCTGTTGCTCCGACAGGGTCAATCAGTTATCTTTCTTCTTGTACTCCGAGCC  
TTCAACCGGTTGTATCACCTGTCGAAGTACGCAAGGAAGGAGCACTGGGG  
AGGGTTTATGTAGCTGCTTATAAGATTGATGCAGATAATTATGTCTACTAC  
AAAAAAGGAGCTTATGAAGTGGGATCTGAGGCGATTATCAATATTGCAGC  
TGCCGCTCAAAAACACATTGATCAAGCTATTTCGTAAACGCTTTTCATGAC  
AGATCAAGCAACTACGCGAGATTTAAATAAAGCCTATATTCAAGCATTTA  
AACAAAAATGTGCCTCTATTTATTATGTACGAGTGAGACAGGACATCCTAG  
AAGGTAGCGAGAGTTATGATGATATGCTGGATGATTTCACTTCATCGGACT  
TAGAAGACTGTCAATCCTGCATGATTAA

(SEQ ID NO: 236)

>KLVQSIKEIGLANAHLAVAPTGSISYLSSCTPSLQPVVSPVEVRKEGALGRV  
YVAAYKIDADNYVYYKKGAYEVGSEAIINIAAAAQKHIDQAISLTLFMTDQAT  
TRDLNKA YIQAFKQKCASIYYVRVRQDILEGSESYDDMLDDFTSSDLEDQCSC  
MI\*

Sequence description:

A] Length 486 bp - 162 aa (Partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-87 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-87 gene sequence. N-terminus to be determined.

ID-196

Clone RS-59(ID-90b)

(SEQ ID NO: 237)

GTGAGGACATATATTACAAACTTGAATGGACATTCAATCACTAGTACAGC  
ACAAATAGCTCAAAACATGGTAACAGATATAGCAGTAAGCTTAGGTTTTC  
GTGAGCTGGGAATACATTCTTATCCGATTGATACTGATTCTCCTGAGGAAA  
TGAGTAAGCGTTTAGATGGAATCTGTTCCGGACTTAGAAAAAATGATATTG  
TCATATTTTCAGACACCTACATGGAACACTACAACCTTTTGATGAAAAATTAT  
TTCACAAATTAAAAATATTTGGTGTAAGATTGTTATTTTTATACATGATGT  
TGTACCGCTAATGTTTGATGGAAATTTTTATTTGATGGATAGAACTATAGC  
TTATTATAATGAAGCAGATGTTTAATAGCCCCTAGTCAAGCAATGGTCGAT  
AAGCTT

(SEQ ID NO: 238)

MRTYITNLNGHSITSTAQIAQNMVTDIAVSLGFRELGIHSYPIDTDSPEEMSKRL  
DGICSGLRKNDIVIFQTPTWNTTTFDEKL FHKLKIFGVKIVIFIHDVVPLMFDGN  
FYLMDRTIAYYNEADVLIAPSQAMVDKL

Sequence description:

A] Length: 414 bp - 138 aa(partial gene)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-90 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-90 gene sequence.

No obvious signal peptide, but a possible Shine Dalgarno sequence is present upstream of ATG start codon. C-terminus has yet to be determined.

ID-197

Clone RS-59c (ID-90c)

(SEQ ID NO: 239)

CATGGAAATGAAGTTGATGATGTTATTAGAAGGGCATTGGAATATAATCAC  
CTTATCTTTGCTTTTGATAATACCTGTCATAACAGAGAGTTAGTATTAGATA  
5 GCAATATCATTCTCACACAACCTGTGAACAATTGATAAATTTAATGAAAA  
ATTTATCAGGCTCCATTATGTATTTGCTAGAGCAACAAAGAGAACAACA  
AGTAATGAAACAAAAGAGCGTTATAAAGAAATATTAGGAGGGTATGGAA  
ATGCCTAA

(SEQ ID NO: 240)

10 HGNEVDDVIRRAFEYNHLIFAFDNTCHNRELVDSNIISHTTCEQLINLMKNLS  
GSIMYLLEQQREQTSNETKERYKEILGGYGNA\*

15 Sequence description:

A] Length: 261 bp - 87 aa(partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was  
20 identified upstream of the ID-90 gene which was identified by LEEP, during  
cloning and sequence analysis of the full-length ID-90 gene sequence. N-  
terminus has yet to be determined

ID-198

25 Clone RS-70b (ID-93b)

(SEQ ID NO: 241)

30 ACATTTTTATATTATGTATTTGAAGACGTAGCCACCCAGTCAAATATGACT  
GGGAAGATTTTATAGTATGTCTAAAGAAGAGTTGTCATATTTACCCGTTATT  
AAACTTTTAAAGAATCAAGGTGTATACAACGGCTTGATTGGTCTATTCCTC  
CTTTATGGGTATATATTTACAGAATCAAGAAATTGTAGCTATTTTTTTAA  
TCAATGTGTTGCTAGTTGCTGTTTATGGTGCTTTGACAGTTGATAAAAAAA  
TCTTATTAAAACAGGGTGGTTTACCTATATTAGCTCTTTTAACATTCTTATT  
35 TTAA

(SEQ ID NO: 242)

TFLYYVFEDVATQSNMTGKIFSMSKEELSYLPVIKLFKNQGVYNGLIGLFLLY  
40 GLYISQSQEIVAIFLINVLLVAVYGALTVDKKILLKQGLPILALLTFLF\*

Sequence description:

A] Length: 312 bp - 104 aa (partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence.

5 N-terminus has yet to be determined

#### ID-199

10 Clone RS-70c (ID-93c)

(SEQ ID NO: 243)  
ATGAAATTAAGTGTCTTGATTATGGGCTTATTGATTATGGAAAACTGCA  
AGTGATGCAATACAAGAAACGATTCTTTTATCACAAGAGGCGGAGCAACT  
AGGCTATCATCAATTTTGGGTGGCTGAACATCACGGTGTTAAGGCATTTCAG  
15 TATTAGCAATCCAGAATTAATGATAATGCATTTGGCTAACCAGACTAAATC  
TATCAAAATTGGCTCTGGAGGTATAATGCCTCTGCACTATAGTAGTTTTAA  
ACTCGCGGAGACTCTCAAGACATTAGAGACATGTCATCCGAATCGAGTAA  
GTATTGGTTTtaggaaattccactagggacagTTAAAGTTTCAAATGCACTTC  
GTAGCTTACATAAAGCACATGATTACGAAGAGGTACTGGAGGAATTGAAG  
20 TCATGGCTTATTGATGAATCATCCAGTAAGGAACCATTAGTTCAACCGACT  
CTTTCTAGCTTCCCAGACTTATATGTGTTGGGGAGTGGTCAAAAATCAGCT  
TATTTAGCGGCTAAACTTGGCTTAGGCTTTACCTTCGGTGTTTTTCTTTTA  
TGGACAAAGACCCATTGACAGAAGCTAAA

(SEQ ID NO: 244)  
25 MKLSVLDYGLIDYGKTASDAIQETILLSQEAEQLGYHQFWVAEHHGVKAFFSIS  
NPELMIMHLANQTKSIKIGSGGIMPLHYSSFKLAETLKTLETCHPNRVSIGLGN  
SLGTVKVSNALRSLHKAHDYEEVLEELKSWLIDESSSKEPLVQPTLSSFPDLV  
LGSGQKSAYLAAKLGLGFTFGVFPFMDKDPLEAK

30

Sequence description:

A] Length: 588 bp - 196 aa (partial)

35 B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence. No obvious signal peptide, but Shine Dalgarno sequence upstream of the ATG start codon.



Figure 3

nucS1

Bgl II Eco RV

5'-cgagatctgatatctcacaaacagataacggcgtaaataag -3' (SEQ ID NO: 245)

nucS2

Bgl II Sma I

5'-gaagatcttccccgggatcacaaacagataacggcgtaaataag -3' (SEQ ID NO: 246)

nucS3

Bgl II Eco RV

5'-cgagatctgatatctcacaaacagataacggcgtaaataag -3' (SEQ ID NO: 247)

nucR

Bam HI

5'-cgggatctcttatggacctgaatcagcgttgtc -3' (SEQ ID NO: 248)

NucSeq

5'-ggatgctttgtttcagggtgtatc -3' (SEQ ID NO: 249)

pTREP<sub>F</sub>

5'-catgatatcggtacctcaagctcatatcattgtccggcaatggtgtgggctttttttgttttagcggataa  
caatttcacac -3' (SEQ ID NO: 250)

pTREP<sub>R</sub>

5'-gcggtatcccccggygcttaattaatgtttaaacactagtcgaagatctcgcgaattctcctgtgtgaatt  
gttatccgcta -3' (SEQ ID NO: 251)

pUC<sub>F</sub>

5'-cgccagggtttttcccgatcacgac -3' (SEQ ID NO: 252)

V<sub>R</sub>

5'-tcaggggggcgagacctatg -3' (SEQ ID NO: 253)

V<sub>1</sub>

5'-tcgtatgtttgtgtggaattgtg -3' (SEQ ID NO: 254)

V<sub>2</sub>

5'-tccggctcgtatgtttgtgtggaattg -3' (SEQ ID NO: 255)

Figure 4

pTREP-Nuc vectors allow cloning of genomic DNA into each frame with respect to the nuclease gene

5

(i)

pTREP1-nuc1 (EcoRV)	AAGTATCAGATCT-- <u>GATATC</u> --TCACAAACAGATAACCGCGTAAAT	Frame=+1
(SEQ ID No: 256)	..... ▲ .....	
pTREP1-nuc2 (Sma I)	AAGTATCAGATCTTCCCGGGA--TCACAAACAGATAACCGCGTAAAT	Frame=+2
(SEQ ID No: 257)	..... ▲ .....	
pTREP1-nuc3 (EcoRV)	AAGTATCAGATCT-- <u>GATATCCATC</u> ACAAACAGATAACCGCGTAAAT	Frame=+3
(SEQ ID No: 258)	..... ▲ .....	
Nuclease Gene	TCACAAACAGATAACCGCGTAAAT	
	(SEQ ID No: 259)	

Cloning site is indicated by an arrow

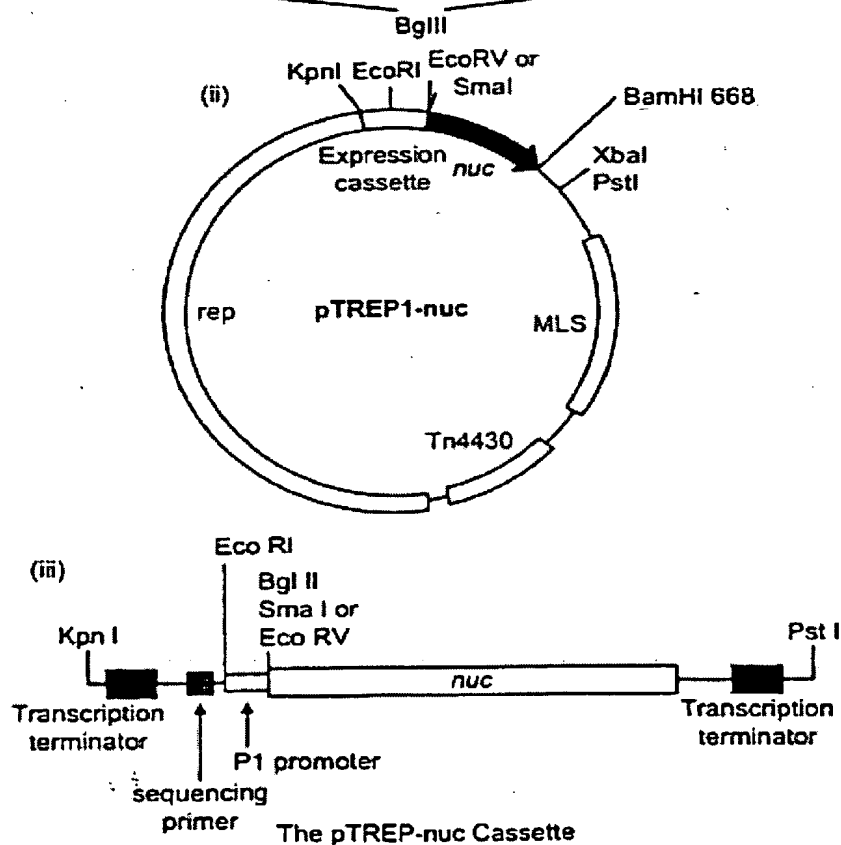
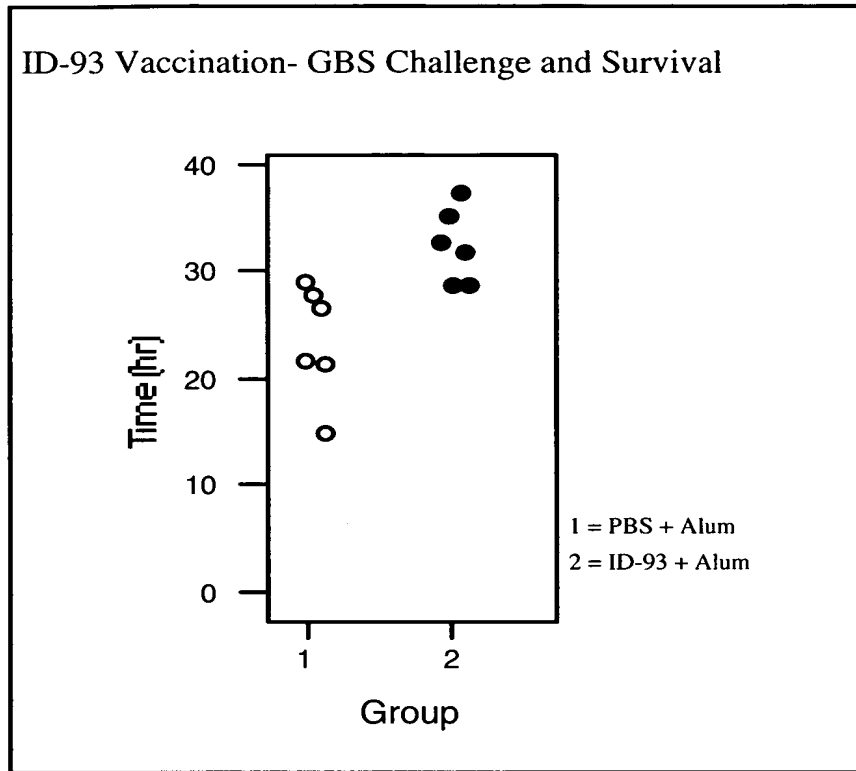


Figure 9  
Survival Data



~~FIGURE 9 SURVIVAL DATA~~